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(without alignments)
697.011 Million cell updates/sec
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1 MTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

SUMMARIES

	Description	Himman SGPOO3	A human requiator	Human phosphatase	Amino acid sequenc	Human ORFX ORF2098	Human cardiovascul	Murine phosphatase	Human polypeptide	Human DSP-7. Homo	Human dual specifi	Human polypeptide
	ID	AAE04837	AAB18667	AAB73219	AAY68779	AAB42334	AAY92177	AAB73214	AAM39977	AAB28519	AAY85620	AAM39356
	DB	22	51	22	21	21	21	22	22	21	21	22
	Query Match Length DB	220	221	198	248	318	221	198	327	291	211	211
ф	Query Match	99.8	88.4	40.1	40.1	40.1	39.9	39.7	39.7	39.3	38.3	38.3
	Score	1159	1026.5	465.5	465.5	465.5	463.5	461	460.5	456.5	445	445
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/note= "Encoded by CTG"

WO200146394-A2

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445 38.3 21 443.5 38.3 21 444.5 38.3 32.4 445.5 38.3 32.5 7 42.5 38.2 20.8 136.3 20.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 346.5 29.8 18 18 20.8 17.7 18 18 20.8 17.7 18 20.8 17.8 1	70 0 0 0 0 0 0 0
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	2 6 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6

ALIGNMENTS

Parkinson's disease; multiple sclerosis; amyorrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskineala; attention disorder; copition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immuosuppressive; antipsoriatic; analgesic; hypotrensive; antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome CHR10. Human, SGP003 phosphatase polypeptide; phosphatase related disease; immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematpoietic cancer; mood disorder; cardiant; J. 173
Jabel- Catalytic_domain
Domain
54..199
Alabel- Phosphatase_domain
Misc-difference 85 Human SGP003 phosphatase polypeptide. AAE04837 standard; Protein; 220 AA (first entry) Homo sapiens. 10-SEP-2001 AAE04837; AAE04837 RESULT

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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal associated diseases and metabolic disorders, including cancers of tissues, cancers of hematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is human Scp003 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP curron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                 Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
                                                                                                                                                                                          Hill RJ;
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1; Mismatches
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                                                                           99US-0173255.
99US-0175766.
2000US-0178078.
2000US-0179301.
                                              21-DEC-2000; 2000WO-US34736
                                                                                                                                                                                       Plowman GD, Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 99.5
mes 219; Conservative
                                                                                                                                                                                                                                     WPI; 2001-418058/44.
N-PSDB; AAD09495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 AA;
                                                                                                                                                           (SUGE-) SUGEN INC.
                                                                                            28-DEC-1999;
25-JAN-2000;
31-JAN-2000;
                                                                           21-DEC-1999;
                28-JUN-2001
                                                                                                                                                                                                          Flanagan P;
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stroke; myeloma;
                                                                                                                                                                                                                                                                                                             /note= "tyrosine specific protein phosphatase active
                                     Human; intracellular phosphorylation regulator; HRIP; stroke; myelon neurotogical disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; myasthenia gravis; cell proliferative disorder; actinic keratosis;
                                                                             arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; autofimune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma.
                                                                                                                                                                                                                                                                                       /note= "potential phosphorylation site"
146..158
                                                                                                                                                                                         "potential phosphorylation site"
                                                                                                                                                                                                           "potential phosphorylation site"
                                                                                                                                                                                                                                                    "potential phosphorylation site"
                                                                                                                                                                                                                                                                       /note= "potential phosphorylation site"
208
                                                                                                                                                                     /note= "potential phosphorylation site"
                                                                                                                                                                                                                               "potential phosphorylation site"
                 A human regulator of intracellular phosphorylation.
                                                                                                                                           Location/Qualifiers
2
                                                                                                                                                                                                                                                                                                                        site"
22-JAN-2001 (first entry)
                                                                                                                                                                                                                                                   /note= "
170
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WO200055332-A2 21-SEP-2000 17-MAR-2000; 2000WO-US07277.

99US-0125593. 99US-0135049. 99US-0143188. 09-JUL-1999; 18-MAR-1999; 20-MAY-1999;

(INCY-) INCYTE PHARM INC

Hillman JL, Baughn MR, Azimzai Y; Yue H, Tang YT, Au-Young J; Bandman O, Lu DAM,

WPI; 2000-602121/57. N-PSDB; AAA75684 Novel human intracellular phosphorylation regulator polypeptides and polynucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders

Claim 1; Page 84-85; 96pp; English.

The present sequence represents a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are useful for treating a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or diagnosed include neurological disorders such as stroke, Parkinson's disease, demyelinating diseases, bacterial and viral meningitis and other developmental disorders of the central nervous system, enromanceular disorders, mysathenia gravis, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, horn marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases, allergies, bronchitis, diabetes mellitus,

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AAB18667 standard; Protein; 221

AAB18667

AAB18667

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Gaps

Indels

Length 198;

DB 22;

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glioblastoma, colorectal cancer and thyroid cancer, pathophysiological hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan Zonana syndrome, schizophrenia and hamartomas.
                                                                                                                                                                                                                                                                                                               PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                                                                                                                                                                       SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human phosphorylation effector PHSP-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder.
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                                                                                                                                                                                          40.1%; Score 465.5; DB 2
48.9%; Pred. No. 2.6e-46;
iive 36; Mismatches 58
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98US-0152814.
98US-0173482.
98US-0106889.
98US-0109093.
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nes 91; Conserv
                                                                                                                                           198 AA;
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03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
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14-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; Moebius, syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
                                                                                                                                                                                                                                                     KLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPT-- 118
                                                                                                                                                                                                                                                                    --FDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                        New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders
                                                                                                                                                                                        1 MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lioubin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to phosphatase proteins and coding
                                                                                                                              Length 221;
                                                                                                                                                           7;
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                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                            VAKNRCVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEEDGREL 220
                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis, microbial infection and trauma.
                                                                                                                             DB 21;
                                                                                                                                           Pred. No. 4.4e-112;
1; Mismatches 12;
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                                                                                                                              Score 1026.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human phosphatase LOC51207_h.
                                                                                                                           Query Match 88.4%;
Best Local Similarity 91.1%;
Matches 204; Conservative
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                                                                                221 AA;
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                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                  (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not yearen in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiatrinic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianeamic; gene therapy; cancer; proliferative disorder; hypotension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
                                                                                                                                                                                                                   treatment
                                                                                      YT, Corley NC, Guegler KJ, Baughn MR;
Au-Young J, Gorgone GA, Yue H, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY68769-95 and AAY68797-99 represent human phosphorylation effectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                                                                                                           human phosphorylation effectors useful for the diagnosis, t
prevention of proliferative, immune and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.1%; Score 465.5; DB 21; Length 248; 48.9%; Pred. No. 3.7e-46; Live 36; Mismatches 58; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              with increased PHSP expression/activity.
                                                                                                                                                                                                                                                                  Claim 1; Page 91; 142pp; English.
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                                                                                    Lal P, Tang YT,
99US-0173482.
99US-0229005.
                                                                                                      Bandman O, A
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                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                        WPI; 2000-183125/16.
                                                                                                                     Reddy R, Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 AA;
                                                                                                                                                                            N-PSDB; AAZ46148
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12-JAN-1999;
12-JAN-1999;
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                                                                                                    Patterson C,
                                                                                    Hillman JL,
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nociropic; neuroprotective; cytopathic; anticonvulsant; antiarthritic; immunosuppressant; limunostimulant; cardiant; thrombolytic; cytopathic; vasotropic; antidiabetic; hypotensive; dermatological: immunosuppressive; antidiabetic; hypotensive; or predisposition to, or preventing or treating the proteins and nucleic acids may be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, dlabetes mellitus, cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, auticimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinifilammatory disease; to enhance company disease; to enhance company disease; and as a contraceptive.
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
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48.9%; Pred. No. 5.3e-46;
ive 36; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 3392-3393; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-602362/57.
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                                                                                                                                                                                                                                        WO200058473-A2
                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1999;
                                                                                                                                                                                                                                                                                                                       05-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cardiovascular system associated protein tyrosine phosphatases are used in the diagnosis and treatment of e.g. immune disorders, anti-proliferative disorders, metabolic disorders and cardiovascular
                                                                                                                                                                                                                                                                Human cardiovascular system associated protein tyrosine phosphatase 4.
                                                                                                                                                                                                                                                                                                             Cardiovascular system associated protein tyrosine phosphatase 4; CSAPTP-4; cytostatic; immunomodulatory; antidiabetic; virucide; hypotensive; cardiant; tyrosine phosphatase modulator.
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/note= "phosphatase catalytic active domain" 164.169
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/label- N_terminal_domain
/note- "unique"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                   AAY92177 standard; Protein; 221 AA.
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98US-0164193.
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312 gretgr 317
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30-SEP-1998;
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Domain
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to determine efficacy of a treatment procedure. CSAPTP nucleic acids, antibodies and protein molecules can be used in screening assays and in predictive medicine e.g. prognostic assays, monitoring clinical trials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
                                                                                                                                                                                                                                                                                FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                        New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders
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                                                                                                                                       39.9%; Score 463.5; DB 2
50.0%; Pred. No. 5.3e-46;
iive 34; Mismatches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whyte D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine phosphatase AA144705_m.
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                                                                                                                                                         Best Local Similarity 50.08
Matches 90; Conservative
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                                                      and pharmacogenetics.
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                                                                                      221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73214;
                                                                                       Sequence
                                                                                                                                           Query Match
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(CEPT-) CEPTYR INC
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25-MAY-1999;
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                                                                                                                                                                                                                            Query Match
Best Local S.
Matches 91
                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                   141
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AAB28519
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hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan Zonana syndrome, schizophrenia and hamartomas.
                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
                                                                                                                                                   81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                               Gaps
                                                                                                              22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                             SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren F, V
Zhang J;
                                                                                              4;
                                                                          Length 198;
                                                                                            59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qian XB,
Yang Y,
                                                                         39.7%; Score 461; DB 22;
49.7%; Pred. No. 8.9e-46;
tive 32; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen R, Ma Y, (Xu C, Xue AJ, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen R,
                                                                                                                                                                                                                                                                                          AAM39977 standard; Protein; 327 AA
                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 3122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Asundi V, CP
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
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2000US-0693036
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                                                                                            94; Conservative
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N-PSDB; AAI59133.
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                           201 VQQRRRSQR 209
                                                                                                                                                                                                                                             ---rretgr 197
                                              198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia.
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Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                             AAM39977;
                                               Sequence
                                                                                             Matches
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous inities, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Labrahmer's parkinson's disease, mutingon's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||: : | | | |:|| | : |::||| |::|| | |: | pkihgavqaspyqpptlaslqrllwvrqaatlnhidevwpslflgdayaardkskliqlg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitogen-activated protein kinase; MAP kinase; dual-specificity phosphatase; DSP-7; cytostatic: immunosuppressive; antiallergic: apoptosis modulation; gene expression modulation; buchenne muscular dystrophy; cancer; graft-versus-host disease; autoimmune diseases; allergy; metabolic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG
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48.9%; Pred. No. 2.1e-45;
iive 35; Mismatches 59
                                                                       ID NO 3122; 10078pp; English
such as central nervous system injuries
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99US-0135757
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                                                                       Example 4; SEQ
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Homo sapiens
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                                                                                                                                   The present sequence is given in a method relating to the isolation of dual-specificity mitogen-activated protein kinase (MAPK) phosphatase DSP-7. The antibody specific to DSP-7 and the antisense polynucleotide of the nucleic acid encoding DSP-7 are useful for detecting DSP-7 expression in a sample which comprises an RNA or cDNA preparation. The antibody is linked to a support material and a detectable marker and the amount of DSP-7 polynucleotide hybridisation assay. The isolated DSP-7 polynucleotide is determined using PCR or hybridisation assay. The isolated DSP-7 polynucleotide is useful for screening agents that modulate DSP-7 activity. The identified agents are useful for treating buchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dual specificity phosphatase-9; DSP-9; human; cytostatic; cell growth; immunosuppressive; antiallergic; antiproliferative; autoimmune disease; cancer; graft-versus-host disease; allergy; metabolic disorder.
                                                       Novel dual-specificity mitogen-activated protein kinase phosphatase polypeptide used in assays to identify agents that modulate the enzyme's activity, which are useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                              81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                                                                         284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human dual specificity phosphatase-9 (DSP-9) amino acid sequence.
                                                                                                                                                                                                                                                                                                                           DB 21; Length 291;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                          Score 456.5; DB 21;
Pred. No. 5.3e-45;
6; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY85620 standard; Protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                  Claim 1; Fig 2A; 70pp; English.
                                                                                                                                                                                                                                                                                                                          39.3%;
48.4%;
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                                                                                                                                                                                                                                                                                                                                               Conservative
                             WPI; 2000-679377/66.
                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                         291 AA;
           Wei B;
                                           N-PSDB; AAC62749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 VQQRRR 206
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                                                                                                                                                                                                                                                                                                                                               90;
           Luche RM,
                                                                                                                                                                                                                                                                                           Sequence
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Matches
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Included in the invention are an expression vector comprising a polynucleotide encoding the DSP-9 protein, a host cell transformed by the expression vector, and an antibody that specifically binds to DSP-9. DSP-9 has cytostatic; immunosuppressive; antiallargic; and antiprolliferative activity. DSP-9 modulating agents are useful for modulating a proliferative response, differentiation or survival of a cell which displays contacting inhibition of cell growth, anchorage independent growth or an altered intercellular adhesion property, in a patient. DSP-9 agonists and antiagonists are also useful for treating a disorder associated with DSP-9 activity such as Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune disease, allergies, metabolic disease, abnormal cell growth, abnormal cell cycle abnormalities. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                   Dual specificity phosphatase-9 which dephosphorylates activated mitogen-activated protein kinase, used to identify agents that inhibit DSP-9 activity and modulate cell proliferation, differentiation, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to an isolated dual specificity phosphatase-9 (DSP-9) and its variant. The DSP-9 protein has the ability to dephosphorylate an activated mitogen activated protein (MAP) kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
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164 laylmlyhhltlveaikkvkdhrgiipnrgflrqllaldrrlrg 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.3%; Score 445; DB 21;
llarity 54.3%; Pred. No. 7.4e-44;
Conservative 26; Mismatches 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim i; Fig 2A; 66pp; English.
99US-0128203
                                                                                                                                                                                                              WPI; 2000-656232/63.
N-PSDB; AAC61100.
                                                                       (CEPT-) CEPTYR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 89; Conserv
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07-APR-1999;
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                                                                                                                                              Luche RM,
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Human SGP060 phosphatase polypeptide
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Best Local Similarity
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8p11.1-q11.1
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  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed
                                                                                                                                                                              Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP 98
                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                             Ren F, W
Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
38.3%; Score 445; DB 22; Length 211;
Best Local Similarity 54.3%; Pred. No. 7.4e-44;
Matches 89; Conservative 26; Mismatches 47; Indels
                                                                                                                                                                             Oian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
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Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 2501; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE04839 standard; Protein; 211 AA
                                                                                                                                                                            Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                             20000S-0598042.
20000S-06598042.
20000S-0653450.
20000S-0662191.
2000US-0693036.
                                        26-DEC-2000; 2000WO-US34263
                                                            2000US-0488725
2000US-0552317
                                                                                                                                  2000US-0727344
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                                                                                                                                                                                                                   WPI; 2001-442253/47.
N-PSDB; AAI58512.
                                                                                                                                                                            Liu C,
Wang 2,
                                                                                                                                                                                                Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AA;
                                                                                                                                                       (HYSE-) HYSEQ INC.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification.
                                                                                                                         19-OCT-2000;
29-NOV-2000;
                                                                                           19-JUL-2000;
                                                                                                    03-AUG-2000;
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                                                            21-JAN-2000;
25-APR-2000;
                                                                                 09-JUL-2000;
                    26-JUL-2001
                                                                                                                                                                                      Wang J, 1
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                            Tang YT,
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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haematopoietic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypetension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amine acid sequence is human Scp060 phosphatase (DSP) and MAP chins of the present as equence is classified as dual specificity phosphatase (DSP) and MAP chins of the present and the present and prosphatase (MKP). SGP060 gene maps to chromosomal position Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; dyostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypotrensive; antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome 8p11.1-q11.1 Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders. immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematopoietic cancer; mood disorder; cardiant; SGP060 phosphatase polypeptide; phosphatase-related disease; Martinez R, Whyte D, Manning G, Sudarsanam S, 61..204 /label- Phosphatase_domain /label= Catalytic_domain Location/Qualifiers Claim 7; Fig 2; 186pp; English. 99US-0173255. 99US-0175766. 2000US-0178078. 2000US-0179301. 21-DEC-2000; 2000WO-US34736 WPI; 2001-418058/44. (SUGE-) SUGEN INC. N-PSDB; AAD09497 WO200146394-A2. 31-JAN-2000; sapiens. 5-JAN-2000; 21-DEC-1999; Plowman GD, Flanagan P; 28-DEC-1999; 28-JUN-2001 Domain Domain Homo

Hill RJ;

Length 211;

Score 445; DB 22; Pred. No. 7.4e-44;

38.3%; 54.3%;

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                                                                         DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                 Gaps
                                                  FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
           5,
           47; Indels
                                                                                                                                                                                                                                 LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
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164 laylmlyhhltlvealkkvkdhrglipnrgflrgllaldrrlrg 207
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    AAM42355 standard; Protein; 328 AA
, 26;
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2000US-0251479
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           Conservative
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13-OCT-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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05-DEC-2000;
05-DEC-2000;
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17-NOV-2000;
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01-DEC-2000;
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14-JUL-2000;
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08-DEC-2000;
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         89;
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           Matches
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The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM42347-AAM4215) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and owher cancers of the adrenal pland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune (thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
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                                                                                                                                                                                                                    Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
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                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 88; 532pp + Sequence Listing; English.
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38.3%; Score 445; DB 22;
Best Local Similarity 54.3%; Pred. No. 1.4e-43;
Matches 89; Conservative 26; Mismatches 47;
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                                    Ruben SM;
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                                    Barash SC,
                                                                                                            WPI; 2001-476225/51.
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                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
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173 AIQQVAKNRCVLPNRGFLKQLRELDKQLVQQRRR 206
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Best Local S:
Matches 87,
                                                                                                                                               AAB28793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various products and methods useful conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, metabolic disorders, including cancers of tissues, cancers of haematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, coular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is human SGPO14 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP kinase phosphatase (MKP). SGPO14 gene maps to chromosomal position
                                                                                                                                                                                                                                                                                                                                                                           RJ;
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                                                                                                                                                                                                                                                                                                                                                                           Hill
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                                                                                                                                                                                                                                                                                                                                                                           Manning G,
                                                                          37.181
/label- Phosphatase_domain
368.520
/label- Phosphatase_domain
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                                                            /label= Catalytic_domain
                            Location/Qualifiers
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                                                                                                                                                                                                                                                          99US-0173255.
99US-0175766.
2000US-0178078.
2000US-0179301.
                                                                                                                                                                                                                            21-DEC-2000; 2000WO-US34736
                                                                                                                                                                                                                                                                                                                                                                        Martinez R,
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N-PSDB; AAD09496.
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                                                                                                                                                           WO200146394-A2
Homo sapiens,
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31-JAN-2000;
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28-DEC-1999;
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Flanagan P;
                                                                                                                                                                                          28-JUN-2001
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New human hydrolase-like molecules (HHLMS) and polynucleotides encoding
the HHLMS, useful for diagnosing, treating or preventing cell
proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to isolated and purified cDNA encoding a human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The HHLM DNAs and polypeptides are useful for diagnosing, treating or preventing cell proliferation disorders and autoimmune disorders. Cell proliferation disorders include cancers, autoimmune disorders include AIDS (acquired immune deficiency syndrome): The present sequence is a HHLM protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
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                                                                                                                                                                                                Hydrolase-like molecule; human; cell proliferation disorder; autoimmune; cancer; AIDS; acquired immune deficiency syndrome
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Pred. No. 1.2e-41;
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                                                                                                                                                  Human hydrolase-like molcule 4 protein.
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53.0%;
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AAB28793 standard; Protein;
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AX180880 Sequence
BC001613 Homo sap1
AX180879 Sequence
AX086020 Sequence
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AX086020 Sequence
AX086010 Sequence
AX013115 Homo sap1
BC003115 Homo sap1
BC003115 Homo sap1
AX113043 Sequence
AX086010 Sequence
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AX086010 Sequence
AX180973 Sequence
I19731 Sequence
I105147 Human dual
BC005682 Homo sap1
AF280809 Mus muscu
AX180923 Sequence
I105147 Human DNA
AX180923 Sequence
AC01579 Homo sap1
AC18490 Drosophil
AL518837 Human DNA
AL451050 Homo sap1
AC01849 Drosophil
AC01849 Drosophil
AC01849 Drosophil
AC01849 Bresquence
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AX063177 Sequence
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AC013088 Homo sap1
AC013186 Drosophil
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Sequence 5 from Patent WO0146394.
AX180878 GI:15132706
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AF280809
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BC003115
AR113043
AX086010
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AX180878
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Result
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                                              ; Search time 1322.25 Seconds
(without alignments)
14535.235 Million cell updates/sec
                                                                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                          1472140 seqs, 8248589755 residues
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Maximum Match 100%
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SUMMARIES

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Catarrhini; Hominidae;
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Genome Therapeutics Corporation Sequencing
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Pred. No. 1.4e-100;
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/clone="RPI1-77G23"
/clone_lib="RPCI-11"
32772 c 34285 g 47356
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Street, Waltham, MA 02453, USA
On May 7, 2000 this sequence versic
Location/Qualifiers
e 1.159517
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Submitted (13-DEC-1999) Genome
Street, Waltham, MA 02453, USA
3 (bases 1 to 159517)
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Street, Waltham, MA 02453, USA
4 (bases 1 to 159517)
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Mammalia, Eutheria, Primates;
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les 605; Conserv
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Pred. No. 1.3e-194;
0; Mismatches 19;
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/db_xref="taxon:9606"
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98.2%;
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/db_xref="GI:15072533" /translation="MAETSLPELGEDKATPCPSILELEELLRAGKSSCSRVDEWPN LFIGDAATANNRFELMAAHRGINCOGGPDFYGSSVSYLGYPAHDLPDFD ISAYESSAADFIHRALNTPCAKVLVHCVVGVSRSATLVLAYLMLHQRLSLRQAVITVR QHRWYPPNRGFLHQLCRLDQQLRGAGOS" misc_feature 5081491 /note="similar to testis- and muscle-expressed dual-specificity protein phosphatase, long form; TMDP-L" misc_feature 8951491 /note="similar to testis- and muscle-expressed dual-specificity protein phosphatase, short form; TMDP" BASE COUNT 329 a 545 c 510 g 342 t	Query Match Best Local Similarity 63.4%; Pred. No. 3.5e-29; Matches 335; Conservative 0; Mismatches 190; Indels 3; Gaps 1; Matches 335; Conservative 0; Mismatches 190; Indels 3; Gaps 1; Matches 335; Conservative 0; Mismatches 190; Indels 3; Gaps 1; Matches 335; Conservative 0; Mismatches 190; Indels 3; Gaps 1; Matches 335; Conservative 0; Mismatches 190; Indels 3; Gaps 1; Matches 335; Conservative 0; Mismatches 190; Indels 3; Gaps 1; Matches 325 troggaagggaaggaaggaactacactacactacactacact	16.	5 COLOR OF STANDARD OF STANDAR	LOCUS AXIBUBENO 636 bp DNA PAT 06-AUG-2001 LOCUS AXIBUBENO 636 bp DNA ACESSION AXIBOBEN 1 GI:15132708 ACCESSION AXIBOBEN 1 GI:15132708 ACESSION AXIBOBEN 1 GI:15132708 KEYWORDS HUMAN ORGANISM HOMO sapiens CORGANISM HOMO sapiens BUARATYOKE: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 636) AUTHORS Plowman, G.D., Martinez, R., Whyte, D., Manning, G., Sudarsanam, S., Hill, R. J. and Flanagan, P. TITLE Mammalian protein phosphatases JOURNAL Patent: WO 0146394-A 7 28-JUN-2001;
	Oy 901 cttgttcaacttccccatgtgtgctgggacaggaggacccaggctgccccgggcag 960 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		S BS JBS J	FEATURES 1. 1726 Source //organiam="Homo sapiens" //organiam="Homo sapiens" //db_xref="taxon:9606" //tissue_type="skeletal muscle" //note="Clone isolated by two-hybrid screen of human skeletal muscle proteins interacting with glycogen-branching enzyme" //codon_start=1 //product="branching-enzyme interacting dual-specificity protein phosphatase BEDP" //protein_id="AAK77966.1"

Mon Feb

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591 gtoctggcctacctgatgatcacaaggacatgaccctggtggacgccatccagcaagtg 650
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                 306
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                                                                                                                                      .,
                                                                                                            Length 636;
                                                                                                                                      Indels
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IMAGE:3535215,
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                                                                                                                                     0; Mismatches 168;
                                                                                                         Score 204.2; DB (
Pred. No. 2.1e-28,
                                                       124
                         /organism="Homo sapiens"
/db_xref="taxon:9606"
207 c 182 g 12
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Mammalia, Eutheria, Primates,
1 (bases 1 to 1665)
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location/Qualifiers
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64.8%;
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Direct Submission
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/translation="MCPGNWLWASMTFWARFSRSSRSPVRTRGTLEEMPTVQHPFLN
YELEBELLTTGCHARACHTAGDNAMNRRELREAGITHTMASHSRWRGT
PEAYEGGGIRYLGYBAHDSPAFDMSTHFGPAADFIHRALSOPGGKILYHCAVGVSRSA
TLVLAYLMLYHLTLVEAIKKVKDHRGIIPNRGFLRQLLALDRRRGGLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found
                                                                                                                                                                                                                Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawam Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: TRAL Plate: 8 Row: o Column: 21
Series TRAL Plate: 8 Row: o Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6807668.
Location/Qualifiers
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/clone="MGC:1136 IMAGB:3535215"
/tissue_type="Lung, small cell carcinoma"
/clone_lib="\nffMGC_"
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/protein_id="AAH01613.1"
/db_xref="GI:12804419"
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Pred. No. 1.8e-28;
0; Mismatches 168;
Note of the control of the contro
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                                         BC Cancer Agency,
info@bcgsc.bc.ca
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protein phosphatase.
Homo sapiens cDNA to mRNA.
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoml;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 904)
1 (bases 2). Martinez,R., Whyte,D., Hill,R., Flanagan,P. i
Lioubin,M.
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                             PAT
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Pred. No. 1.6e-27;
0; Mismatches 166;
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                 AXU86020 904 bp DNA
Sequence 17 from Patent W00112819.
AX086020
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 282 c 249 g 19
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Local Similarity 64.3%;
nes 299; Conservative
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1917)
Plowman, G. D., Martinez, R., Whyte, D., Manning, G., Sudarsanam, S.,
Hill, R., J. and Flanagan, P.
Mammalian protein phosphatases
Patent: WO 0146394-A 6 28-JUN-2001;
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880 AAAGACCACCGAGGCATCATCCCCAACCGGGGCTTCCTGAGGCAGCTCCTGGCCCTGGAC 939
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Pred. No. 6.9e-28;
0; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                388
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
596 c 565 g 386
                                                                                                                AX180879 1917 bp DNA
Sequence 6 from Patent W00146394.
AX180879 GI:15132707
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Location/Qualifiers
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Matches 328; Conserv
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/product="protein phosphatase"
/protein_id="aAB109778_1"
/protein_id="14602535"
/d_xref="c01:14602535"
/translation="mosLokopirrrkingavQaSpvQpPTLASLQRLLMVRQAATLNHIDEVWPSLFLGDaYaARDKSKLIQLGITHVVNAAAGKFQVDTGAKFYRGMSLEYYGI
EADDNPFFDLSVYFLPVARYIRAALSYPQGRVLUHCAMGVSRSATLVLAFLMIYENMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: b Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6692781. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadam@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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/tissue_type="Bone marrow, chronic myelogenous leukemia"
  Homo sapiens, protein phosphatase, clone MGC:13471 IMAGE:4047963, mRNA, complete cds.
                                                                                                                                                                                                                                           Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acceacytcaacyagytctygoccaagetctacattygocyatyagygyacygocygyac 335
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298 c 298 g 209 t
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Pred. No. 3e-27;
0; Mismatches 167;
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/db_xref="LocusID:51207"
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                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 1053)
Strausberg,R.
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                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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                                         BC009778
BC009778.1 GI:14602534
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298; Conservative
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                                                                                                                                               Kikuchi, K., Nakamura, K. and Shima, H.
Kikuchi, K., Nakamura, K. and Shima, H.
Subirect Submission
Submitted (07-MAY-1999) to the DDBJ/EMBL/GenBank databases. Kunimi
Kikuchi, Hokkaido University, Section of Biochemistry, Institute of
Immunological Science: Kita-15, Nishi-7, Kita-ku, Sapporo 060-0815,
Japan (E-mail:kikuchi@imm.hokudai.ac.jp, Tel:81-11-707-6839,
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EADDNPFFDLSVYFLPVARYIRAALSVPQGRVLVHCAAGVSRSATLVLAFLMICENMT
LVEAIQTVQARNICPNSGFLRQLQVLDNRLGREFGRF"
284 c 254 g 188 t
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                                       Nakamura, K., Shima, H., Watanabe, M., Haneji, T. and Kikuchi, K. Molecular cloning and characterization of a novel dual-specificity protein phosphatase possibly involved in spermatogenesis biochem. J. 344 Pt J, 819-825 (1999)
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Pred. No. 3.1e-27;
0; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="protein phosphatase"
/protein_id="BAA89412.1"
/db_xref="GI:6692782"
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 298; Conservative
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/translation="WSIHFOTAADFIHRALSOPGGKILVHCAVGVSRSATLVLAYLML
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346 c 379 g 220 t
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Bandman,O., Lal,P., Hillman,J.L., Corley,N.C., Guegler,K.J. and
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 /product="Unknown (protein for MGC:2627)"
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Patent: US 6132964-A 12 17-OCT-2000;
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                  /protein_id="AAH03115.1"
/db_xref="G1:13111895"
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493 c 528 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (13-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                         BCO03115 1243 bp mRNA PRI 12-JUL-2001
Homo sapiens, clone MGC:2627 IMAGE:3502718, mRNA, complete cds.
BC003115
575
                                                                                                                          cggtcagccaccetggtcctggcctacctgatgatccacaaggacatgaccetggtggac 635
                                                                                                                                          559 CGAGCTGCCCTCAGTGTTCCCCAAGGCCGCGTGCTGGTACACTGTGCCATGGGGGTAAGC 618
                                                     gacagagcgctaagcgaccacagtaagatcctggttcactgcgtcatgggccgcagc
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Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC_Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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279. .539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg, R.
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Kikuchi, K., Nakamura, K. and Shima, H.

Direct Submission

Submitted (07-MX-1999) to the DDBJ/EMBL/GenBank databases. Kunimi
Kikuchi, Hokkaido University, Section of Biochemistry, Institute of
Immunological Science; Kita·15, Nishi-7, Kita-ku, Sapporo 060-0815,
Japan (E-mail: kikuchi@imm.hokudai.ac.jp, Tel:81-11-707-6839)
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LVDAIQTVQAHRDICPNSGFLRQLOVLDNRLRREFGRL.
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Nakamura,K., Shima,H., Watanabe,M., Haneji,T. and Kikuchi,K.
Molecular cloning and characterization of a novel dual specificity
protein phosphatase possibly involved in spermatogenesis
Biochem. J. 344 Pt 3, 819-825 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                          411 cccgactactaccgcgacatggacatccagtaccacggcgtggaggccgacgacctgccc 470
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                                                                                                      CAGCTGGGCATTACCCATGTTGTGGGCTGCGGCCAAGTTCCAGGTGGACACAGGT
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1. .597
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 597)
Plowman, G.D., Martinez, R., Whyte, D., Hill, R., Flanagan, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 gtctggcccaagctctacattggcgatgaggcgacggcggctggaccgctataggctgcag 350
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                   Gaps
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                 Indels
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 4.9e-23;
ches 165;
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Pred. No. 4e-21;
); Mismatches 213;
 Pred. No. 4.9e.
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Sequence 7 from Patent WO0112819.
AX086010
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63.0%;
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 Best Local Similarity 63.0
Matches 312; Conservative
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EADDNPFFDLSVHFLPVARTRDALAVIPRSRVLVHCAMGVSRSATIVLAFLMIFENMT

LVDAIQTYQAHRDTOPNSGFLKQLOVLDNRERFGRL

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imates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.5e-21;
Mismatches 213; Indels 0;
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                                                   280 acytcaacyagytctggcccaagctctacattggcgatgaggcgacggctggaccgct 339
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                            Gaps
                          9:
    Length 4360;
Score 145.8; DB 6; Length
Pred. No. 1.1e-17;
0; Mismatches 207; Indels
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Query Match 12.5%;
Best Local Similarity 58.2%;
Matches 296; Conservative
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Sequence 8, A Sequence 5, A Sequence 5, A Sequence 2, A Sequence 20, A Sequence 20, A Sequence 23, Sequence 2, A Sequence 1, A Sequence 13, Sequence 13, Sequence 13, Sequence 11, A Seque

Sequence

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APPLICANT: Acton, Susan
TITLE OF INVENTION: No. 6268135el Phospholipase Molecule and Uses Therefor
FILE REPERENCE: mni-059
CURRENT APPLICATION NUMBER: US/09/163,833
CURRENT FILING-DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 PKIHGAVQASPYQPPTLASLQRLLMVRQAATLNHIDEWWPSLFLGDAYAARDKSKLIQLG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 SKILVHÇVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.1%; Score 465.5; DB 4; Best Local Similarity 48.9%; Pred. No. 2.8e-46; Matches 91; Conservative 36; Mismatches 58;
                         US-08 446 363-3
US-08-015 985-8
US-08-144 925-5
US-08-015-986A-2
US-08-144 925-5
US-08-15-986A-2
US-08-164 193-2
US-09-164 1193-2
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US-09-041-886-13
US-08-015-973-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09013881
Patent No. 6132964
GENERAL INFORMATION:
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 116
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2308
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CORGANISM: Homo sapiens
US-09-163-833-2
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LENGTH: 198
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Sequence 2, Appli
Sequence 25, Appli
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                                                                                                                                                                          US-09-847-519A-2
1161
1 WTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEDGREL 220
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Sequence 2,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-164-193-5
US-09-164-193-5
US-09-164-193-21
PCT-US93-12019-2
US-09-980-379-4
US-08-990-379-4
US-08-990-379-5
US-08-990-379-5
US-08-990-379-5
US-08-990-379-5
US-08-990-379-6
US-08-990-379-6
US-08-990-379-8
US-08-993-750C-21
US-08-933-750C-21
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                                                                                                                                                                                                                                                                                           212252 segs, 22503292 residues
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                                                                                                             8, 2002, 15:40:01
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Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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1185
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Post-processing:

Database

Title: Perfect score:

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Scoring table:

Searched:

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1; Gaps

Bandman, Olga Lal, Preeti Hillman, Jennifer L. Corley, Neil C. Guegler, Karl J.

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Sequence Sequence Sequence Sequence Sequence Sequence

166 157.5 142.5 142.5 128.5 123 103.5 100.5

346.5 346.5 346.5 346.5 2247.5 1927.5 11927.5 1188.5 1777.5

Result Š

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41 LERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDY 100
                                                                                                                                                                                                                                                          101 YRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLA 160
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                                                                                                Query Match 31.3%; Score 363; DB 4; Length 263; Best Local Similarity 51.8%; Pred. No. 3.6e-34; Matches 73; Conservative 22; Mismatches 44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AARONSON, Stuart A.
APPLICANT: BOTTARO, Donald P.
APPLICANT: ISHIBASHI, Toshio
APPLICANT: MIKI, Toru
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN
TITLE OF INVENTION: PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,273
FILING DATE: 19921214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 346.5; DB 1;
Pred. No. 1.8e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/07988273
Patent No. 5512434
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Foley & Lardner: 3000 K Street, N.W., Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATMAE: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                             123 YLMLYHHLTLVEAIKKVKDHR 143
                                                                                                                                                                                                                                                                                                                                      161 YLMIHKDMTLVDAIQQVAKNR 181
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TELECOMMUNICATION INFORMATION:
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43.8%;
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TELEFAX: (202)672-5399
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AMINO ACID
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Best Local Similarity 43.89
Matches 78; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLCY & L
                  ORGANISM: Homo sapiens
JS-09-164-193-5
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CLASSIFICATION:
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US-07-988-273-2
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Patent No. 6258582
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amended FILE REFERENCE: MNI-051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 4; Length 207; 1.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 LAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 LAYLMLYHHITLVBAIKKVKDHRGIIPNRGFIRQLIALDRRLRQ 203
              TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES WUBBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: .
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 1.2e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 263
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                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
                                                                                          Palo Alto
                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid
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Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: MUSCNOT02
CLONE: 971204
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                          USA
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APPLICANT:
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US-09-164-193-5
                                                                                                                                                        COUNTRY:
                                                                                            STREET:
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US-09-013-881-4
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Sequence 21, Applior
Patent No. 6258582
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JS-09-164-193-21
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              88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                 88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GSFELSVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 185;
                                                                                                                                                                                                                                                                                  Catalytic Macro Molecules Having DCD25B
Like Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5;
1.8e-32;
54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 346.5;
; Pred. No. 1.8e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                 3: Pharmacia & Upjohn Company
301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     Sequence 25, Application US/08848810 Patent No. 6074851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Wootton, Thomas A.
REGISTRATION NUMBER: 35,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-7914
TELEFAX: 616-833-6897
                                                                                                                                                                                                                                APPLICANT: Deibel Jr., M.R.
APPLICANT: Yen, A.W.
APPLICANT: Wilson, C. L.
TITLE OF INVENTION: Catalytic
TITLE OF INVENTION: Like Activ
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 43.89
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                       US-08-848-810-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-848-810-25
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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RESULT

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GENERAL INFORMATION:
APPLICANT: ACLON, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amerILE REFERENCE: MNI-051
CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATEHILIN Ver. 2.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                37 GAFE----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 GAFE----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                 Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXPRESSION CLONING OF A HUMAN PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 346.5; DB 5;
; Pred. No. 1.8e-32;
35; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                            29.8%; Score 346.5; DB 4
43.8%; Pred. No. 1.8e-32;
ive 35; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US93/12019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,273
FILING DATE: 14-DEC-1992
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9312019 GENERAL INFORMATION:
Application US/09164193C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 amino acids
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Best Local Similarity 43.8%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.89
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PHOMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-09-164-193-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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RESULT

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GENERAL INFORMATION:
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Missae Phosphatase CDNAs and
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Their Biologically Active Expression Products
TITLE OF INVENTION: Their Biologically Active Expression Products
FILE REFERENCE: 4104 000322USA
CURRENT PELING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: PCT/US96/10402
EARLIER APPLICATION NUMBER: 60/00,263
EARLIER FILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 VLNAAHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAA-AFIDRALSDDH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 EILPFLYLGSAXHAARRDMLDALGITALLNVS-----SDCPNHF-EGHYQYKCIPVEDN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 PIFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADIFIDQALAQKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELD 197
                                                                                                                                                                                                                                                                                                                                                                                                    Length 118;
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                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                21.3%; Score 247.5; DB 5; llarity 47.0%; Pred. No. 3e-21; Conservative 24; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 34.2%; Pred. No. 4.4e-14;
Matches 50; Conservative 29; Mismatches 58;
                                                                                             PCT/US93/12019
                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,273
FILING DATE: 14-DEC-1992
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
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                                                                                                                                                                                                                                                         : 118 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Rattus norvegicus
                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            PCT-US93-12019-3
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US-08-990-379-4
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63 AEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADIFIDQALAQKN 60
                                                                        146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
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                                                                                                                                                                                                                                        GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: AARONSON, Stuart A.
APPLICANT: BOTTARO, Donald P.
APPLICANT: ISHIBASHI, Toshio
APPLICANT: MIKI, Toru
TITLE OF INVENTION: PHOSPHATASE
TITLE OF INVENTION: PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSION CLONING OF A HUMAN PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40399/182 NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,273 FILING DATE: 19921214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9312019
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                       Sequence 3, Application US/07988273
Patent No. 5512434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 40
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20007-5109
COMPUTER READABLE FORM:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
PCT-US93-12019-3
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Sequence 7, Application US/08990379

Sequence 7, Application US/08990379

Patent No. 5998188

GENERAL INFORMATION:

APPLICANT: Stork, Philip J

APPLICANT: Misra-Press, Anita

TITLE OF INVENTION: Microgen Activated Protein Kinase Phosphatase CDNAs and

TITLE OF INVENTION: Microgen Activated Protein Kinase Phosphatase CDNAs and

TITLE OF INVENTION: Microgen Activated Protein Kinase Phosphatase CDNAs and

TITLE OF INVENTION: Microgen Activated Protein Kinase Phosphatase CDNAs and

TITLE OF INVENTION: Microgen Activated Protein Kinase Phosphatase CDNAs and

TITLE OF INVENTION: Microgen Activated Protein Kinase Phosphatase CDNAs and

CURRENT APPLICATION NUMBER: US/08/990,379

CURRENT FILING DATE: 1997-12-15

EARLIER PILING DATE: 1995-06-16

NUMBER OF SEQ ID NOS: 19

NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELER-----LFWKGSPQYTHV 55
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Misra-Press, Anita
APPLICANT: Misra-Press, Anita
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase CDNA,
TITLE OF INVENTION: The Endography Active Expression Products
TITLE OF INVENTION: The Endography Active Expression Products
FILE REFERENCE: 4104-0003220sA
CURRENT APPLICATION NUMBER: US/08/990,379
CURRENT FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: 60/000,263
EARLIER PILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 16.6%; Score 192.5; DB 2; 11 Similarity 34.2%; Pred. No. 4.4e-14; 50; Conservative 29; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
16.2%; Score 188.5; DB 2;
Best Local Similarity 28.0%; Pred. No. 9.2e-14;
Matches 58; Conservative 39; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Rattus norvegicus US-08-990-379-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus sp. US-08-990-379-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-990-379-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                     APPLICANT: Marshall, Christopher John
APPLICANT: Marshall, Alan
APPLICANT: Ashworth, Alan
APPLICANT: Hughes, David Anthony
TITLE OF INVENTION: Methods for Screening of Substances for
TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 192.5; DB 2
; Pred. No. 4.4e-14;
29; Mismatches 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/00694
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-DEC-1995
CLASSIFICATION: 435
IOR ADDITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 9402573.1
FILING DATE: 10-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9307250.2
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 : | : : | | : | : |: | 335
310 VKQRRSIISPNFSFMGQLLQFESQVL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 23, Application US/08530290 Patent No. 5958721 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bastian, Kevin L.
REGISTRATION UNDBER: 34,774
REFERENCE/DOCKET NUMBER: 0846
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08990379; Patent No. 5998188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.2%;
Matches 50; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-530-290-23
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                  California
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US-08-990-379-5
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80 GFTHVLNAA----HGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 LSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 GITCIVNATIEIPNFNW-----PQF-----EYVKVPLADMPHAPIGLYFDTVADKI-HS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 177.5; DB 4;
; Pred. No. 8.9e-13;
33; Mismatches 61;
OPERATING SYSTEM: DOS SOFTWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/045,973 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 8, 2002, 15:42:02
                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0491 US
                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; 28.5%;
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 15.3
Best Local Similarity 28.5
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT16
; CLONE: 3041794
US-09-045-973-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:/ single
TOPOLOGY: linear
                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 ELDKQL 200
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160 DYERQL 165
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TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amended FILE REPERENCE: MNI-051
CURRENT PELLOR NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
   174 -EILPYLYLGSCNHSSDLQGLQACGITAVLNVS-----ASCPNHFEGL-FHYKSIPVED 225
                                                                       116 LPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQ 175
                                                                                                              226 NOMVEISAWFQEAISFID-SVKNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFD 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GSCNHSSDLOGLOACGITAVLNVS-----ASCPNHFEGL-FHYKSIPVEDNQMVEISAW 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 FYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | :||| ::| | :||| | | ||||| | |||||| : | :| | | : | || : | || : | || : | || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 184.5; DB 4; Length 314; 28.3%; Pred. No. 2.7e-13; Live 39; Mismatches 84; Indels 19
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APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                        176 QVAKNRCVL-PNRGFLKQLRELDKQLV 201
| : | |: | |: | : |: |: 285 FVKQRRGVISPNFSFMGQLLQLETQVL 311
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-164-193-22
. Sequence 22, Application US/09164193C
. Patent No. 6258582
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-045-973-5; Sequence 5, Application US/09045973; Patent No. 6165767
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 -PNRGFLKQLRELDKQLV 201
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APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-09-164-193-22
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CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

protein - protein search, using sw model

8, 2002, 15:43:46; Search time 23.54 Seconds February Run on:

(without alignments) 692.274 Million cell updates/sec

US-09-847-519A-2

score: Perfect

220 1 MTSGEVKTSLKNAYSSAKRL.....VQQRRRSQRQDGEEEDGREL 220 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

522463 segs, 74073290 residues Searched:

10 Word size :

Total number of hits satisfying chosen parameters:

7

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human SGP003 phosp	A human requlator	Human SGP014 phosp	Human polypeptide	Human hydrolase-li	Human dual specifi	Human polypeptide	Human SGP060 phosp	Human cardiovascul	Human polypeptide	Human SGP014 phosp
	ID	AAE04837	AAB18667	AAE04849	AAM41142	AAB28793	AAY85620	AAM39356	AAE04839	AAY92175	AAM42355	AAE04838
	DB	22	21	22	22	22	21	22	22	21	22	22
	Query Match Length DB	220	221	57	80	207	211	211	211	263	328	549
æ	Query Match	61.4	44.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5
	Score	135	86	12	12	12	12	12	12	12	12	12
	Result No.		7	3	4	Ŋ	ø	7	ω	6	10	11

ALIGNMENTS

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Human; SGP003 phosphatase polypeptide; phosphatase-related disease; infimune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pdin; sexual dysfunction; Alzhedmar's disease; metabolic disorder; haematopoletic cancer; mood disorder; cardiant; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neurological disorder; virucide; nootropic; cerebroprotective; therapy; hypotensive; immunosuppressive; antipsoriatic; antisthmatic; antistingal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome CHR10.
                                                                          Human SGP003 phosphatase polypeptide.
          AAE04837 standard; Protein; 220 AA
                                                      (first entry)
                                                      10-SEP-2001
                                  AAE04837;
AAE04837
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Homo sapiens.

54..199 /label- Phosphatase_domain /label = Catalytic_domain Location/Qualifiers Domain Domain

/note- "Encoded by CTG" 82 Misc-difference

WO200146394-A2

28-JUN-2001

21-DEC-2000; 2000WO-US34736

21-DEC-1999; 99US-0173255, 28-DEC-1999; 99US-0175766, 25-JAN-2000; 2000US-0178078, 31-JAN-2000; 2000US-0179301.

(SUGE-) SUGEN INC.

R.J.; Martinez R, Whyte D, Manning G, Sudarsanam S, Hill Plowman GD, Flanagan P;

WPI; 2001-418058/44. N-PSDB; AAD09495.

Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal associated diseases and metabolic disorders

Claim 7; Fig 2; 186pp; English.

The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by

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17-MAR-2000; 2000WO-US07277
                            18-MAR-1999;
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prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dysfunesias and organ transplant rejection. The present amino acid sequence is human SGPO03 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (BSP) and MAP Kinase phosphatase (MKP). SGPO03 gene maps to chromosomal position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stroke; myeloma;
                                                                                                                                                                                             86 NAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                                                                                                                                          146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQRR 205
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "tyrosine specific protein phosphatase active
    site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; intracellular phosphorylation regulator; HRIP; stroke; myelon neurological disorder: Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; maysthenia gravis; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; autoimmune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma.
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                                                                                                                                               Length 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note- "potential phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A human regulator of intracellular phosphorylation.
                                                                                                                                             61.4%; Score 135; DB 22; I
100.0%; Pred. No. 5.3e-128;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          AAB18667 standard; Protein; 221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "potential
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                                                                                                                                                                     Matches 135; Conservative
                                                                                                                                                                                                                                                                                          206 RSQRQDGEEEDGREL 220
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                                                                                                                                                           Local Similarity
                                                                                                            220 AA;
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                                                                                                             Sequence
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                                                                                                                                               Query Match
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AAB18667
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The present sequence represents a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist or antagonist or antagonist or antagonist or antagonist. An adversarial of a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or decreased include neurological disorders such as stroke, Parkinson's other developmental disorders of the central nervous system, neuromuscular disorders of the central nervous system, neuromuscular disorders, myasthenia gravis, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases, allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial infection and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive;
                                                                                                                                                                                                                                                                                                                                 Novel human intracellular phosphorylation regulator polypeptides and polynucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWP 60
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                                                                                                                                                                         Baughn MR, Azimzai Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 98; DB 21; Lred. No. 1.1e-90; Mismatches 0;
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                                                                                                                                                                      Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 84-85; 96pp; English.
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100.0%; Pre
0;
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99US-0125593.
99US-0135049.
99US-0143188.
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Best Local Similarity 100.
Matches 98; Conservative
                                                                                                               (INCY-) INCYTE FHARM INC
                                                                                                                                                                   Tang YT,
                                                                                                                                                                                                  Au-Young J;
                                                                                                                                                                                                                                                WPI; 2000-602121/57.
N-PSDB; AAA75684.
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                            20-MAY-1999;
09-JUL-1999;
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amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Wang Z, F
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AA;
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                                                                                                    WO200153312-A1.
                                                                                                                                                                                                                                         09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                 29-NOV-2000;
                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                               14-SEP-2000;
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25-APR-2000;
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                                                                                                                                        26-JUL-2001
                                     leukaemia.
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Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is human SGP014 phosphatase polypeptide related exon.
SGP014 sequence is classified as dual specificity phosphatase (DSP) and MAP kinase phosphatase (MKP). SGP014 gene maps to chromosomal position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haemacopoletic origin, diseases of central and peripheral nervous system. Alzheimer's disease, Parkinson's disease, multiple sclerosis, ammyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fund, coular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders; cognition
                                                                                                                                                                                                                                                                                                                                                                                              Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
                                                                                                                                                                                                                                                                                                             Hill RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; curopathy; central nervous system; CNS; Alzheimer's; Parkinson's.disease; Huntington's disease; haemostatic;
antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome 10q21.3; exon 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to phosphatase polypeptides, nucleotide
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                                                                                                                                                                                                                                                                                                               Sudarsanam S,
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Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                               Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 127; 186pp; English
                                                                                                                                                                                                                                                                                                             Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM41142 standard; Protein; 80 AA.
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100.0%; Pre
0;
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                                                                                                                                                                                       99US-0173255.
99US-0175766.
2000US-0178078.
2000US-0179301.
                                                                                                                                                    21-DEC-2000; 2000WO-US34736.
                                                                                                                                                                                                                                                                                                           Plowman GD, Martinez R,
Flanagan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 SRSATLVLAYLM 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 AA;
                                                                                  WO200146394-A2
                                                                                                                                                                                     21-DEC-1999;
28-DEC-1999;
25-JAN-2000;
31-JAN-2000;
                                                    Homo sapiens.
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                                                                                                                    28-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                             Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \dot{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                          Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                    Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 6073; 10078pp; English.
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                                                                                                                                               2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
26-DEC-2000; 2000WO-US34263
                                                                                                                2000US-0598042
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 SRSATLVLAYLM 163
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26 srsatlvlaylm 37
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N-PSDB; AA160298.
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26-JUL-2001
         Luche RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia
                                                                                                                                                                                                                                                                                                Sequence
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                                                                                     survival
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                                                                                                                                                                                                 New human hydrolase-like molecules (HHLMs) and polynuclectides encoding the HHLMs, useful for diagnosing, treating or preventing cell proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
                                                                                                                                                                                                                                                                The present invention relates to isolated and purified cDNA encoding a human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The HHLM DNAs and polypeptides are useful for diagnosing, treating or preventing cell proliferation disorders and autoimmune disorders. Cell proliferation disorders and autoimmune disorders. Cell ALDS (acquired immune deficiency syndrome). The present sequence is a HHLM protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dual specificity phosphatase-9; DSP-9; human; cytostatic; cell growth; immunosuppressive; antiallergic; antiproliferative; autoimmune disease; cancer; graft-versus-host disease; allergy; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                     Guegler KJ, Shah P, Lal P, Corley NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human dual specificity phosphatase-9 (DSP-9) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                        ;
        Hydrolase-like molecule; human; cell proliferation disorder; autoimmune; cancer; AIDS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                     5.5%; Score 12; DB 22; Length 207; 100.0%; Pred. No. 0.00052; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             Claim 1; Column 47-48; 38pp; English.
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                                                                                            98US-0013881
                                                                                                              98US-0013881
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Matches 12; Conservative
                                                                                                                                 (INCY-) INCYTE PHARM INC
                                                                                                                                                   Bandman O, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                           152 SRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-006133/01
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                                                                                                                                                                                                                                                                                                                                          207 AA;
                                                                                                                                                                                N-PSDB; AAC60226
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                                     Homo sapiens
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                                                                                            06-FEB-1998;
                                                                                                              06-FEB-1998;
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                                                       US6132964-A.
                                                                          17-0CT-2000
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This invention relates to an isolated dual specificity phosphatase-9 (DSP-9) and its variant. The DSP-9 protein has the ability to dephosphorylate an activated mitogen activated protein (MAP) kinase.

C dephosphorylate an activated mitogen activated protein (MAP) kinase.

C included in the invention are an expression vector comprising a polynucleotide encoding the DSP-9 protein, a host cell transformed by the expression vector, and an antibody that specifically binds to DSP-9.

DSP-9 has cytostatic; immunosuppressive; antiallargic; and antiprollferative response, differentiallargic; and modulating a prollferative response, differentiallard of a cell which displays contacting inhibition of cell growth, anchorage independent growth or an altered intercellular adhesion property, in a patient. DSP-9 activity such as Duchenne muscular disorder associated with DSP-9 activity such as Duchenne muscular disorder associated with DSP-9 activity such as Duchenne muscular collected; metabolic disease, abnormalicell growth, abnormal cell prowth, abnormal cell cycle abnormalities. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                          Dual specificity phosphatase-9 which dephosphorylates activated mitogen-activated protein kinase, used to identify agents that inhibit DSP-9 activity and modulate cell proliferation, differentiation, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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100.0%; Pred. No. 0.00053;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                Claim 1; Fig 2A; 66pp; English.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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Best Local Similarity 100.0
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WPI; 2000-656232/63.
N-PSDB; AAC61100.
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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Domain
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                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system, such as paripheral nervous system, such as paripheral nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, heamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, as a says for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; SGP060 phosphatase polypeptide; phosphatase-related disease; infimune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer*s disease; metabolic disorder; heematopoietic cancer; mood disorder; cardiant; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; actiousscular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; antischmatic; antigraine; chromosome #pli.1-q11.1.
                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                            Ren F, War Zhang J;
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                                                                            Qian XB,
Yang Y,
                                                                           Asundi V, Chen R, Ma Y, (
Mehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                           Example 4; SEQ ID NO 2501; 10078pp; English.
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                                                                            Liu C, Asundi V,
Wang Z, Wehrman T,
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2001 (first entry)
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                                                                                                      zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AA;
                                                   (HYSE-) HYSEQ INC
                                                                                                                                             N-PSDB; AAI58512
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C.N.S disorders.
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                                                                                          Wang J, W
Zhao QA,
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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase conditions. Substance that modulates the activity of phosphatase conditions. Substance that modulates the activity of phosphatase collapsed is used to treat immune-related diseases and disorders, nactuding cancers of tissues, cancers of metabolic disorders, including cancers of tissues, cancers of haematopoietic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral: infections, infections caused by prions, bacteria and fungi, coular diseases, diabetes, migraines, parkinson's disorders, hypotension, hypertension, psychotic disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is classified as dual specificity phosphatase (DSP) and MAP condition of the properties of the propert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cardiovascular system associated protein tyrosine phosphatase 2; CSAPTP-2; cytostatic; immunomodulatory; antidiabetic; virucide;
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Pred. No. 0.00053;
0; Mismatches 0;
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                                                                              61..204
/label- Phosphatase_domain
1..173
/label- Catalytic_domain
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99US-0175766.
2000US-0178078.
2000US-0179301.
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N-PSDB; AAD09497.
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28-DEC-1999;
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Flanagan P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cardiovascular system associated protein tyrosine phosphatases are used in the diagnosis and treatment of e.g. immune disorders, anti-proliferative disorders, metabolic disorders and cardiovascular
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223..225
Anote= "Protein Kinase C phosphorylation site"
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te= "Protein Kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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hypotensive; cardiant; tyrosine phosphatase modulator.
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176..179
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98US-0164193.
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a neural disorder, a cardiovascular disorder e.g. hypertension or coronary heart disease or a disorder rising from improper phosphorylation of a phosphorylated protein. Anti-CSAPTP antibodies are used to isolate CSAPTP by standard techniques, to facilitate the purification of natural and recombinantly produced CSAPTP from cells, to detect CSAPTP protein in cell supernatant for evaluating the level of CSAPTP expression and to monitor protein levels in tissue as part of a clinical testing procedure to determine efficacy of a treatment procedure. CSAPTP nucleic acids, antibodies and protein molecules can be used in screening assays and in predictive medicine e.g. prognostic assays, monitoring clinical trials
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100.0%; Pred. No. 0.00065;
ive 0; Mismatches 0;
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01-DEC-2000;

MKP; migraine; chromosome 10q21.3.

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adream gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune hammolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
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                          05-DEC-2000; 205-DEC-2000; 206-DEC-2000; 208-DEC-2000; 208-DEC-2000; 211-DEC-2000; 208-DEC-2000; 208
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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of metabolic disorders, including cancers of tissues, cancers of hematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, saxual dysfunction, mood disorders, attention disorders, conlition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present anno acid sequence is human ScPO14 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
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o. 0.0013; Indels
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                                                                                                               /label= Phosphatase_domain
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Location/Qualifiers
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99US-0175766.
2000US-0178078.
2000US-0179301.
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                                                                                                                                             ..520
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nes 12; Conservative
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Job time: 120 sec
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N-PSDB; AAD09496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUGE-) SUGEN INC.
                                                                                                                                                                                                                               WO200146394-A2
                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-1999;
28-DEC-1999;
25-JAN-2000;
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OM protein - protein search, using sw model

Run on:

February 8, 2002, 15:45:01 ; Search time 15.43 Seconds
(without alignments)
1086.092 Million cell updates/sec

US-09-847-519A-2 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description esult Query No. Score Match Length DB ID n to a

No matches found

Result

Search completed: February 8, 2002, 15:48:10 Job time: 189 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 8, 2002, 15:46:07 ; Search time 11.72 Seconds (without alignments) 688.248 Million cell updates/sec

US-09-847-519A-2
220
1 WISGEVKISLKNAYSSAKRL.....VQQRRRSQRQDGEEEDGREL 220

Title: Perfect score: Sequence:

OLIGO Gapop 60.0', Gapext 60.0 Scoring table:

100059 segs, 36664827 residues

Searched:

10 Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

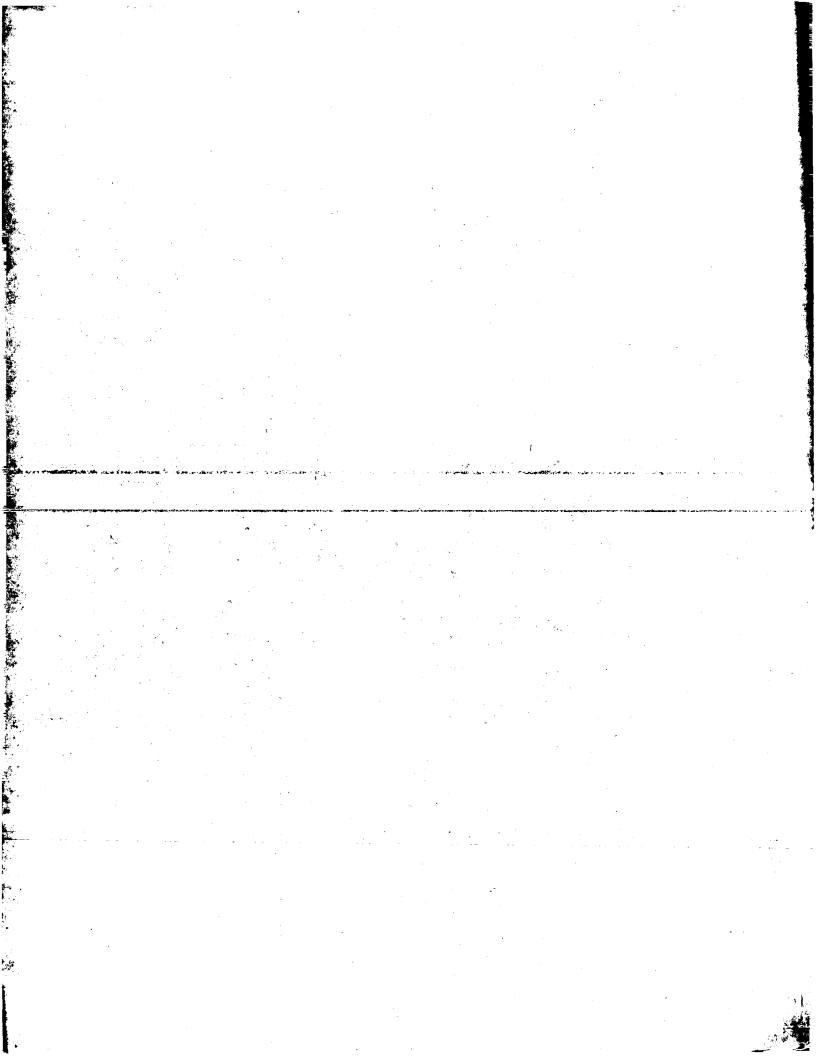
SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description esult Query No. Score Match Length DB Result

No matches found

Search completed: February 8, 2002, 15:49:20 Job time: 193 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2002, 15:45:47; Search time 23.66 Seconds Run on:

(without alignments) 1360.098 Million cell updates/sec

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US-09-847-519A-2 Perfect score:

1 MTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

473505 seqs, 146272329 residues Searched:

10 Word size : rotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 ... Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_17:*

sp_human:*
sp_invertebrate:*
sp_mammal:* sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* sp_fung1:* sp_rodent:* sp_plant:* sp_virus:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_vertebrate:*

SUMMARIES

esult Query No. Score Match Length DB ID Description	Q9btwO homo sapien Q9d700 mus musculu Q9bv47 homo sapien
ΙΩ	86 4 Q9BTW0 198 11 Q9D700 211 4 Q9BV47
DB	4 11 4
Query Match Length DB ID	86 198 211
Query	
Score	122
Result No.	357

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (FOPTEIN FOR MGC:2627).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                             86 AA
ALIGNMENTS
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                                                                             PRELIMINARY;
                                                                        Q9BTW0
Q9BTW0;
                                            RESULT
Q9BTW0
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Gaps

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0; Indels

5.5%; Score 12; DB 11; 100.0%; Pred. No. 0.00035; iive 0; Mismatches 0;

Query Match 5.5 Best Local Similarity 100. Matches 12; Conservative

Length 198;

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Gaps
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                            ö
                                                                                                     Length 86;
                                                                                                                          0; Indels
                                         Strausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003115; AAH03115.1; -. SEQUENCE 86 AA: 9652 MW; 4DD29AFD5989528B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22419 MW; 11F0CAF4B5620F0E CRC64;
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Last annotation update)
                                                                                                      DB 4; Le
0.00017;
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SMART; SM00012; PTPC_DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                          Mismatches
                                                                                                    Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).

EMBL; AK009781; BA226501.1; -

MGD; MGI:1914209; 2310043K02Rik.

InterPro; IPR000340; DS_phosphatase.

InterPro; IPR000387; TYR_phosphatase.

Pfam; PF00782; DSPC; 1.
                                                                                                                                                                                                                                          01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; PubMed-11217851;
                                                                                                    Query Match 5.5%; Sox
Best Local Similarity 100.0%; P:
Matches 12; Conservative 0;
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                   SEQUENCE FROM N.A. TISSUE=NEUROBLASTOMA;
                                                                                                                                              152 SRSATLVLAYLM 163
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                                                                                                                                                          32 SRSATLVLAYLM 43
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                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
 NCBI_TaxID=9606;
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SEQUENCE
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09D700;
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99BV47 PRELIMINARY; PRT; 211 AA.
09BV47;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1136).
EUKADOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 5.5%; Score 12; DB 4; Length 211; Best Local Similarity 100.0%; Pred. No. 0.00037; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-LUNG CARCINOMA;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001613; AAH01613.1;
SEQUENCE 211 AA; 23945 MW; 60E944304905086D CRC64;
152 SRSATLVLAYLM 163
                      144 SRSATLVLAYLM 155
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Search completed: February 8, 2002, 15:49:02 Job time: 195 sec

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Sequence Sequence

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Sequence 3, Application US/09163833
Patent No. 6268135
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: No. 6268135el Phospholipase Molecule and Uses Therefor
FILE REFERENCE: mni-059
CURRENT APPLICATION NUMBER: US/09/163,833
CURRENT APPLICATION DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 594
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Pred. No. 1.1e-36;
0; Mismatches 166;
                                US-08-869-696-20
US-08-387-942C-19
US-08-387-942C-19
US-08-869-696-21
US-08-869-696-22
US-08-869-696-8
US-08-861-173-508-1
US-08-951-1742-1
US-08-869-696-1
US-08-869-696-1
US-08-869-696-1
US-08-869-696-1
US-08-869-696-1
US-08-81-1742-1
US-09-130-114-2
US-09-320-878-22
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Best Local Similarity 64.3%;
Matches 299; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: (1)..(594)
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                                                                                     Search time 46.06 Seconds (without alignments) 5728.330 Million cell updates/sec
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Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 42, Appli
Sequence 10, Appli
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                                                                                                                                          Description
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
           4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-163-833-1

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US-09-164-193-6

US-09-164-193-4

US-09-164-193-4

US-08-273-1

US-08-273-1

US-08-990-379-1

US-08-990-379-1

US-08-941-442-4

US-08-941-442-4

US-08-941-442-1

US-08-139-941-4

US-08-139-941-4

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US-08-139-1

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US-08-139-1
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US-09-196-390-5
                                                                                                                                                                                                                                        351203 seqs, 113238999 residues
        GenCore version
Copyright (c) 1993 - 2000
                                                                                        8, 2002, 17:32:35
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Maximum Match 100%
Listing first 45 summaries
                                                              sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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199.4
175
161.6
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Perfect score:
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Pred. No. 5.1e-31;
0; Mismatches 165; Indels
                                                                                           APPLICANT: Shaĥ, Purvi
TTLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no...
FILING.DATE: um...
                                                                                                                                                                        Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0470 US
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Bandman, Olga
Lal, Preeti
Hillman, Jannifer L
Corley, Neil C.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                    3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.0%;
Best Local Similarity 63.0%;
Matches 312; Conservative
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1691 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: MUSCNOT02;
CLONE: 971204
US-09-013-881-12
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                                                                                                                                                                                                                                                                    94304
                                                                                                                                                                        ADDRESSEE:
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                                                     APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                              STATE:
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TITLE OF INVENTION: No. 6268135e1 Phospholipase Molecule and Uses Therefor
FILE REFERENCE: mni 059
CURRENT APPLICATION NUMBER: US/09/163,833
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                 181 aaccatatcgatgaggtctggcccagcctcttcctgggagatgcgtacgcagcccgggac 240
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gocatocagoaagtggccaagaaccgctgcgtcctcccgaaccggggctttttgaagcag
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Pred. No. 1.2e-36;
0; Mismatches 166;
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                                                                                                                                                                                                          Sequence 1, Application US/09163833 Patent No. 6268135
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Best Local Similarity 64.3%;
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (52)..(645)
US-09-163-833-1
                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-09-013-881-12
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 912
                                                                                                                                                                     RESULT 2
US-09-163-833-1
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GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as ame FILE REFERENCE: MNI-051
CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1016;
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Patent No. 5512434
GENERAL INFORMATION:
APPLICANT: AARONSON, Stuart A.
APPLICANT: BOTTARO, Donald P.
APPLICANT: BOTTARO, Donald P.
APPLICANT: ISHBASHI, TOSHIO
APPLICANT: MIKI, TOSHIO
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.9%; Score 161.6; DB 4; Best Local Similarity 61.9%; Pred. No. 4.8e-28; Matches 276; Conservative 0; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      665 cgtcctcccgaaccggggctttttga 690
                                                Sequence 4, Application US/09164193C Patent No. 6258582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agaggccgaggccactgtca
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                    | NAME/KEY: CDS
| LOCATION: (1)..(789)
| US-09-164-193-4
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US-09-164-193-6
Sequence 6, Application US/09164193C
Sequence 6, Application US/09164193C
Sequence 6, Application US/09164193C
GENERAL INFORMATION:
APPLICAMY: ACTON, SUSAN L.
TITLE OF INVENTION:
FILE REFERENCE: MNI-051
CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 161.6; DB 4;
Pred. No. 4.5e-28;
); Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agaggccgagccccaggccactgtca 457
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llarity 61.9%;
Conservative 0
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                                                                                                                                                           711 aagcagctggtgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (1)..(789)
US-09-164-193-6
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Best Local Simi
Matches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
LENGTH: 789
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CLONING OF A HUMAN

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12019
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,273
FILING DATE: 14-DEC-1992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
uuence 1, Application PC/TUS9312019
SNERAL INFORMATION:
APPLICANT:
                                                                                                NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 56.6
Matches 269; Conservative
                                                              TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
PCT-US93-12019-1
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US-08-530-290-11
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                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,273
CLIAG DATE: 19921214
                                                                                                                                                                                                                                                                                                                                    40399/182 NIHD
                      3000 K Street, N.W., Suite 500 Washington, D.C.
                                                                        ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    ATTORREY, AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40395
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELERAX: (202)672-5399
TELERAX: (202)672-5399
TELERAX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%;
56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 56,6
Matches 269; Conservative
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    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-07-988-273-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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263 cagiccccagitacacccacgicaacgaggictggcccaagcictacaitggcgaigaggc 322
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                                                                 0; Mismatches 200; Indels
11.4%; Score 133; DB 5; 56.6%; Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08530290
Patent No. 5958721
GENERAL INFORMATION:
APPLICANT: Marshall, Christopher John
APPLICANT: Ashworth, Alan
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RESULT 7 PCT-US93-12019-1

us-09-847-519a-1.rni

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Score 60.2; DB 2;
Pred. No. 6.2e-05;
0; Mismatches 158;
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                                                                               Sequence 1, Application US/08990379 Patent No. 5998188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.2%;
Best.Local Similarity 51.1%;
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Rattus norvegicus
US-08-990-379-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best.Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   1987
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                                                            US-08-990-379-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gacyccatccaycaagtggccaagaaccyctgcgtcctcccgaaccggggcttttgaag 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
APPLICANT: Hughes, David Anthony
IITLE OF INVENTION: Methods for Screening of Substances for
IITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.1%; Score 70.6; DB 2; Length 1
Best Local Similarity 52.9%; Pred. No. 2.3e-07;
Matches 176; Conservative 0; Mismatches 154; Indels
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA
                                                      NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  084611-000000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1026 GGGCAGCTGCTGCAGTTCGAGTCCCAGGTGCTG 1058
                                                                                                                                                                                                                                                                                                                                                                                                           PRICE APPLICATION UNBER: WO PCT/GB94/00694
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9402573.1
FILING DATE: 10-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9307250.2
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagctccgggagctggacaagcagctggtgcag 725
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/530,290
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFRENCE/DOCKET NUMBER: 0846
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1238 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA
US-08-530-290-11
                                                                                                                                                                                              94111-3834
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           996
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GENERAL INFORMATION:
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Mista-Press, Anita
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Their Biologically Active Expression Products
TITLE OF INVENTION: Their Biologically Active Expression Products
FILE REPERENCE: 4104-0003228A
FILE REPERENCE: 1997-12-15
CURRENT APPLICATION NUMBER: PCT/US96/10402
EARLIER PPLICATION NUMBER: 60/000,263
EARLIER FILING DATE: 1995-06-16
SOFTWARE: FILING DATE: 1995-06-16
SOFTWARE: Patentin Ver. 2.0 Sequence 2. Application US/08990379
Fatent No. 5998188
GENERAL INFORMATION:
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Misra-Press, Anita
TITLE OF INVENTION: Miscaen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Miscaen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Miscaen Theory That Biologically Active Expression Products
FILE REFERENCE: 4104-00032205A
CURRENT APPLICATION NUMBER: US/08/990,379
CURRENT FILING DATE: 1997-12-15
EARLIER FILING DATE: 1996-06-14
EARLIER FILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19 ä 1289 ggctttcgagttcgtcaagcagcgccgtagcatcatctcgcccaacttcagcttcatggg 1348 1172 agac---gcagtgaaggactgccgagggcgagtgctggttcactgccaggccggcatctc 1228 1052 gaatgteteeteagaetgeeecaateaetttgagggaeattaeeagtaeaagtgeateee 1111 395 gaacgtggacactgggcccgactaccgcgacatggacatccagtaccacggcgtgga 454 cgccatccagcaagtggccaagaaccgctgcgtcctcccgaaccggggctttttgaagca 694 515 cgacagagcgctaagcgacgaccacagtaagatcctggttcactgcgtcatgggccgcag 575 ccggtcagccaccctggtcctggcctacctgatgatccacaaggacatgacctggtgga ë, Length 1987; Indels

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Boulder
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                                                                                                                   TOPOLOGY:
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Best Local 5
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                                                                             TYPE:
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                                                                                                                                                       Length 1993
                                                                                                                                                                                          Indels
                                                                                                                                                   Score 60.2; DB 2;
Pred. No. 6.2e-05;
0; Mismatches 158;
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APPLICANT: SEED, BRIAN
APPLICANT: HASS, JUNGEN
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,294
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20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-717-294-42
; Sequence 42, Application US/08717294
; Patent No. 6114148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-0200
                                                                                                                                                   5.2%;
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                                                     TYPE: DNA
CRGANISM: Rattus norvegicus
US-08-990-379-2
                                                                                                                                                                                        Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                        Similarity
SOFTWARE: Patentin
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                                   LENGTH: 1993
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                 SEQ ID NO 2
                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                 Length 4451;
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PatentIn Release #1.0, Version #1.30
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5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
Annessone
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; Sequence 10, Application US/08941445A
; Patent No. 6107060
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
     42:
                                                                                                                                                                                                                                                               4.48;
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APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starcl
                                                       LENGIH: 4451 base pairs
                                                                                                                                                                                                                                                                                                               Conservative
                               SEQUENCE CHARACTERISTICS
INFORMATION FOR SEQ ID NO:
                                                                             nucleic acid
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US-08-717-294-42
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OPERATING SYSTEM:
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Matches 195; Conserva
                                                                                                                                       linear
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375 aacgeggeecaeggeegetggaaegtggaeattgggeeegaetaetaeegegaeatggae 434
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APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHORCH
                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08387942C Patent No. 5939289
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/CDCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 702-205-8000
INFORMATION SO IN 0: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 base pairs
                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS
                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
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US-08-387-942C-1
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APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: VALLA, SVEIN
APPLICANT: WALLA, SVEIN
APPLICANT: WARENER, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49.8; DB 3; Length 2
Pred. No. 0.014;
0; Mismatches 162; Indels
                 APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY_AGENT INFORMATION:
                                                                  ATTORNEY/AGENT INCOMMENT.

NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2097 base pairs
TYPE: nucleic acid
Anuble
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Patent No. 5939289
                                                                                                                                                                                                                                                                                                                                                                                          CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.6%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                          SS: double
not relevant
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..2097
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                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: not re
MOLECULE TYPE: CDN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 gcagcagag 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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US-08-941-445A-10
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NAME/KEY: CDS
LOCATION: 744..11219
COTHER INFORMATION: /function= "gene= "eryA""
OTHER INFORMATION: /product= ""ORF1 encoding modules 1 & 2 for OTHER INFORMATION: 6-deoxyerythronolide B""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 2250.3626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LCCATION: 744..1868
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 3831..4811 OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase 2 domain of module 1" FEATURE:
                                                             ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /function= "APPROXIMATE SPAN OF OTHER INFORMATION: MODULE 1"
OTHER INFORMATION: /label= FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1998..2198
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 1 of module
FEATURE:
                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/642,734C FILING DATE: 17-JAN-91
                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DANCKETS, ANDREAS M
REGISTRATION NUMBER: 32652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 11219 base pairs
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LOCATION: 744..6659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                   CORRESPONDENCE ADDRESS
                                                                                                                                         Abbott Park
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               842 Tregadadadereceraegechaegeceaegecheegericaaegregecaecaecae 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      902 CACGATTTCGTCATGACCAACAACGTCGCCTACGGCAACGGCAGCGGCGCCTGGTGGTG 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 aaggacatgacctggtggacgccatccagcaagtggccaagaaccgctgcgtcc 669
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APPLICANT: Katz, L
APPLICANT: Donadio.
APPLICANT: Macabine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48.6; DB 2; Length 1
Pred. No. 0.048;
0; Mismatches 154; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: U9-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Azotobacter vinelandii
                                                                                                            FILING DALL.

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURRHY OR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/POCKET NUMBER: 1809-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.8%;
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
6702..9695
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9973..12588
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2227..6438
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290..1951
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US-08-387-942C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10070 GCGGGTGTCGGTGCGCGTGCGACGTCAGCAGCGGAACCGGTGAGGGAACTCGTGCA 10129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10130 CGCCTGATCGAGCAGGCGACGTCGTCGCGGTGTGGTGCACGCGGGGGGACTGCCGCA 10189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10190 GCAGGTCGCGATCAACGACATGCACGAGGCCGCCTTCGACGAGGTGGTCGCGGGCCAAGGC 10249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 ccgcgacatggacatccagtaccacggcgtggaggccgacctgcccaccttcgacct 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 cacgcacgtgctgaacgcggcccacggccgctggaacgtggacactgggcccgactacta 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602 cctgatgatccacaaggacatgacctggtgacgccatccagcaagtggccaagaaccg 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 48.2; DB 1; Length 11219;
45.9%; Pred. No. 0.057;
tive 0; Mismatches 193; Indels 0;
/function= "approximate span of
beta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
COGATION: 9906..10454
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 6678.8066
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacyl ACPSynthase of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 8262..9305
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 2"
                                                                        NAME/KEY: misc_feature
LOCATION: 6369..6626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module 1"
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CCATION: 10707..10964

O'THER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 2"
US-07-642-734C-1
                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 6678..11219
OTHER INFORMATION: /function="approximate span
OTHER INFORMATION: module 2"
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Matches 164; Conservative
OTHER INFORMATION:
OTHER INFORMATION:
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211954 MA 602040965 601813316 AU168945

Title: Perfect score:

Sequence:

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Run

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
and _minmatch 12 options.
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1 (bases 1 to 572)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett C.S., Wardy, J.E., Walte, J., Cho, J., Fahrenkrug, S.C., Bennett C.G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF212271
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AW951243
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                       AK006247
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AW425509
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BF527844
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221711 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BF074326
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BE892660
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FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG Plate: 80 row: I column: 23

PCR PRimers

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401 368 242.4 200 194.4

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Score

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FEATURES

Query Match Best Local S Matches 500

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BASE COUNT ORIGIN

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/lab.host="SOLR"
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Bento Soares"
                                                                                                                                                                                                   USA
                                                                                                     Gene Index (1998)
Unpublished (1998)
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, US. Fax: (301) 838-5229
Fax: (301) 838-5229
Fax: (301) 838-5208
Fax: 
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0; Mismatches 112;
                                        Lee, N.H., Glodek, A., Chandra, I., Mason, T. Kerlavage, A.R. and Adams, M.D. Rat Genome Project: Generation of a Rat
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGCTGGACCGCTATGGGCTGCAGAAGGCAGGCTTCACCCCACGTGCTGAACGCTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ggctgctacatgccccacggaccagaacctcccgacggccaggccccggcacacccag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggcgtggaggccgacctgcccaccttcgacctcagtgtcttcttctacccggcggc
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                                                                                                                                                                                                                                                           1 others
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ches 72;
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                                                                                                                                                                                                                                                                                                                                               Score 444.4; D
Pred. No. 4.1e-
0; Mismatches
                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                adrenal, and endometrium.
187 c 161 g 99
                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC_2Bov"
/tissue_type="pooled"
/lab_host="DH10B"
primer: ATTTAGGTGACACTATAG
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:8084199
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87.0%;
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EST

VERSION KEYWORDS SOURCE ORGANISM

LOCUS

RESULT AW918423

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595 CAAGAACATGA
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                                                                                                                                                    AW918455 605 bp mRNA EST 25-MAY-2000 EST349759 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIES53 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="mix - brain, ovary, placenta, kidney, lung,
liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
Xhol; Estimated insert size approx.1 kb"
192 c 173 g 106 t
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Rat gene index, normalized rat, norvegicus,
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                594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                               (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                              Chandra, I., Mason, T.M., Quackenbush, J.,
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
TTE1: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 401; DB 10; Length 6
Pred. No. 2.4e-62;
0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                           Lee N.H., Glodek,A., Chandra,I., Mason,T.M.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST
                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIES53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                       AW918455
AW918455.1 GI:8084231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 34.4%;
Best Local Similarity 80.9%;
Matches 494; Conservative
                                                                                                                                                                                                                                                                                                                               (bases 1 to 605)
                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
                                                                                                                                                                                                                                                                 norvegicus
                                                                                                                                                                                                                                                   Norway rat.
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                                                                                                                                                                                                                                                                                                                  Rattus.
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
                                                                                                                                                                                 433
                                                                                                                                                                                                                                                                                                                                                                                          553
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25-APR-2001
                                                                                                                                                                                 494 ctaccoggoggoagcottcatcgacagagogctaagcgacgaccacagtaagatcctggt
                                                                         475 CTACTCGGCTGCCGCTTCATCGACTCGGCGCTCCAAGACGACCACAGTAAGATCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcactgcgtcatgggccgcagccggtcagccaccctggtcctggcctacctgatcca
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275868 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF652341
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Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
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Plate: 65 row: K column: 11
Seq primer: ATTTAGGTGACACTATAG.
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/clone_lib="MARC 3BOV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
1 152 c 134 g 84 t
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                            cctcccgacgcggccaggccccggcacacccagctgcagaaaggagagaaaatcccttgg 112
                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                ctggcccaagctctacattggcgatgaggcgacggctggaccgctataggctgcagaa
                                                                                                   3;
                                                                          Length 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE808287 505 bp mRNA EST 2
213454 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE808287 GI:10239399
                                                                                                   60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                         Score 368; DB 11;
Pred. No. 2.1e-56;
                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                       31.6%;
86.9%;
                                                                                    Best Local Similarity 86.9
Matches 417; Conservative
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VERSION
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AUTHORS
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Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       accacagtaagatcctggttcactgcgtcatgggccgcagccggtcagccacctggtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agctgtaggcccgactcacagggccagcagaggcacttgggggacagaggggagagaggcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acatagccctggcctaggact-----ccagagaagggatggtgaaaccgaagctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 AAACAGCTCTGCCCCATGACTTCTTTGTCGCAGAGAGGGACATGAAACCAAAGCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATCACAATAAGATCCTGGTTCACTGCGTCATGGGCCGCCGCGGCGGCGACTCTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agctggtgcagcagaggcgacggtcccagcgccaggacggtgaggaggaggatggcaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTGGTGCAGCAGAGGCGACAGGCCCAGCAGGGTGAGGACGCCGAGAAGTGTGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    886 actottocaaaccatottgttcaacttocccatgtgtgctggggacagggaggacccaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 GTGGGCTCCGGGACGAGGCCGGGGCTTGGCTTCACTGCAAAATGGCGGGACCGGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255994 MARC BSM Bos taurus cDNA 5', mRNA sequence.
BF430044
BF430044.1 GI:11442141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 242.4; DB 11;
Pred. No. 6.1e-34;
0; Mismatches 116;
and -minmatch 12 options.
PCR PRIMETS
FORWARD: AGGAAACAGCTATCACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 67 row: P column: 14
Seq primer: ATTTAGGTGACATAG.
                                                                                                                                                                                      /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                     /organism="Bos taurus"
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.8%;
Best Local Similarity 73.3%;
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486 bp
                                                                                                                                                  1. 505
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/clone_lib="Nii_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="bl108 (phage-resistant)"
/note="Organ: brain: Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAGGG. Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-refmail.nih.gov
Tissue Procurement: Arboration: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1783 row: i column: 24
High quality sequence stop: 701.
Location/Qualifiers
rce
                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 cccgactactaccgcgacatggacatccagtaccacggcgtggaggccgacgacctgccc 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGAGGCCTATGAGGGGCTGGGCATCCGCTACGGTGTTGAGGCCCACGACTCGCCA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCCAGGAGGAAGATCCTGGTGCATTGTGTGTGTGGGCGTGAGCCGATCCGCCACCCTG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtcctggcctacctgatgatccacaaggacatgaccctggtggacgccatccagcaagtg 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcctttgagctggagcggctcttctggaagggcagtccccagtacacccacgtcaacgag 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 gtctggcccaagctctacattggcgatgaggcgacggcgctggaccgctataggctgcag 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 aaggoggggttcacgcacgtgctgaacgcggcccacggccgctggaacgtggacactggg 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gacgaccacagtaagatcctggttcactgcgtcatgggccgcagccggtcagccacctg 590
                                                                                                                                                                                                            1 (bases 1 to 703)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                         602761093F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4896479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 accttcgacctcagtgtcttcttctacccggcggcagccttcatcgacagagcgctaagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 GCCTTTGACATGAGCATCCACTTCCAGACGCTGCCGACTTCATCCACCGGGCGCGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 194.4; DB 1
Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4896479"
                                                                                        BI199835.1 GI:14654856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.7%;
59.6%;
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                                                   mRNA sequence.
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S AUTHORS
S TITLE
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                                                                    ACCESSION
                                                                                        VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Uni-ZAP.XR; Site_1: EcoRI; Site_2: XhoI; Library obtained from Stratagene, catalog #937721. Library ande from skeletal muscle of a two year old Holstein cow." 147 c 136 g 107 t
                                                                                                                                                                                                                                                                                                18
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                                                                       Kata, S.
                                                                                                                                                                                                                                                                        Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.

PCR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tccccagtacacccacgtcaacgaggtctggcccaagctctacattggcgatgaggcgac 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggccgctggaacgtggacactgggcccgactactaccgcgacatggacatccagtacca 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 626 cctggtggacgccatccagcaagtggccaagaaccgctgcgtcctcccgaaccgggctt 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AGGCAAGTITCAGGTGGACACAGGTGCCAAGTICTACCGCGGAATGCCCTTGGAGTACTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 TCGATACATCCGAAGTGCCCTCAGTGTTCCCCAAGGCCGGGGGTGCTGGTACACTGTGCCAT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 TGCCATGTTGAACCATTTCAATGAAGTCTGGCCCAACCTCTTCCTGGGAGACGCGTACGC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-2001
                                                            Marken, W.C., Tao, N., Allison, T., Wagner, S., Mathialagan, N., Johnson, J., Smith, T.P.L. and Womack, J. A survey of genes transcribed in bovine skeletal muscle Unpublished (2000) Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 200; DB 11;
Pred. No. 2.4e-26;
0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="MARC BSM"
/tissue_type="Skeletal muscle"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                      FORWARD: GGAAACAGCTATGACCATG
BACKWARD: GTTTTCCCAGTCACGAC
Seq primer: AATTAACCCTCACTAAAGGG.
                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .486
/organism="Bos taurus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref-"taxon:9913"
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Best Local Similarity 64.4%;
Matches 299; Conservative
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                                             (bases 1 to 486)
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ORIGIN
                                                                                                       TITLE
JOURNAL
COMMENT
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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakwa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno, M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J., Kolima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nouna,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H.,
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                                                  391 GTACTGGCCTACCTCATGCTGTACCACCATCCTTACCCTGGAGGCCATCAAGAAAGTC 450
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The RIKEN Genome Exploration Research Group Phase II Team and
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Nature 409, 685-690 (2001)
5 (bases 1 to 1748)
                                                                               451 AAAGACCACCGAGGCATCATCCCCAACCGGGCTTCTGAGGCAGCTCCTGGCCCTGGAC
                                                                                                                                                       711 aagcagctggtgcagcagaggcgacggtcccagggccaggacggtgaggaggatggc
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Carninci, P. and Hayashizaki,Y.
High-effictency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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/codon_start=1
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TLVFBAIKKVKDHRGITPNRGFLRQLLALDRRLRQGLEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Annial Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGATCCAAGAGCTTTTTTTTTTTTTTTYN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to ROt = 5.0 and subtraction to ROt = 25.0. Second strand cDNA was prepared with the primer adapter
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                            Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute
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/db_xref="MGD:MGI:1895208"
/db_xref="MGD:MGI:1914209"
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, T. L., Grosse, W. M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovinae; Bos. (bases 1 to 558)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        normalized bovine cDNA
                                                                                                                                                                                                                                                                         1022
                                                                                        842
                                                                                                                                                                                                                                          673
                                                                                                                     553
                                                                                                                                                                                613
                                                                                                                                                                                                            962
                            729 CAACGCCTCACACACACAGGTGGCGAGGCACC----CCCGAGGCCTATGAGGGACTGGG 782
                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2001
                                                                         903 GCACTGTGCGGTGGGGGGGGAGCAGCCTACCCTGGTGCTGCTGCTGTA
                                                                                                                                                                                                                                        caaggacatgacctggtggacgccatccagcaagtggccaagaaccgctgcgtcctccc
                                                                                                                                                                                                                                                                      963 TCACCACTTCACCCTTGTGGAGGCCATCAAGAAAGTCAAGGACCACCGAGGCATCACCCC
 gaacgcggcccacgctggaacgtggacactgggcccgactactaccgcgacatgga
                                                           catccagtaccacggggggggggggggggccgacctcgacctcagtgtcttctt
                                                                                                                    494 ctacccggcggcagccttcatcgacagagcgctaagcgacgaccacagtaagatcctggt
                                                                                                                                                                              554 tcactgcgtcatgggccgcagccggtcagccaccctggtcctggcctacctgatgatcca
                                                                                                                                                                                                                                                                                                  libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                          BF077053 558 bp mRNA EST 2
226847 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
BF077053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4360
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue
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180 c 171 g 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
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Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GITITCCCAGICACGACG
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PCR PRimers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 990)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                  380
                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
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                                                                                                                                                                                                   320
                                                                                                                                                                                                                           || | GGGAAGGTTTCTTCCAGCCACGTGGAGTTTGGCCCAACCTTTACATAGGAGATGGG 167
                                                                                                                                                                                                                                                                                                                                  gcccacggccgctggaacgtggacactgggcccgactaccgcgacatggacatccag 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 CTCTCCCTGCGCCAGGCGGTGATCACCGTGAGGGAGCGCCGATGGGTCTTCCCCCAACAGA 524
                                                  Gaps
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                                                                                                 ggggaggaggactactgcaccctggagcctttgagctggagcggctcttctggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                    taccacggcgtggaggccgacgacctgcccaccttcgacctcagtgtcttcttctacccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggcagtccccagtacacccacgtcaacgaggtctggcccaagctctacattggcgatgag
                                                                                                                                                                                                                                                                                                     gegacggettggaccgctataggetgcagaaggeggggttcacgcacgtgctgaacgeg
                                               3,
Length
                                                  Indels
Score 187.6; DB 11;
Pred. No. 3.8e-24;
                                               0; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GETTECTTCACCAGCTCTGCCGGCTGGACCAGC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggctttttgaagcagctccgggagctggacaagc 714
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High quality sequence stop: 582.
Location/Qualiflers
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF207232 990 bp mRNA 601870679F1 NIH_MGC_19 Homo s
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/clone="IMAGE:4100947"
/clone=lib="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/tasue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain, Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1104)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           47 IGGAGCGCTCCTCTACACAGCAAGACAGCCTGTAACCATGCCGACGAGGTCTGGCCAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 agctctacattggcgatgaggcgacggcgctggaccgctataggctgcagaaggcggggt 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTCTATCTCGGAGACCAGGACATGGCTAACAACCGCCGGGAGCTTCCCGCCT-GGGCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAGGGCTGGGCATCCGCTACCTGGGTGTTGAGGCCCACGACTCGCCATGGCTTGACA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 gctgcgtcctcccgaaccggggctttttgaagcaqctccgggagctggacaagcagctgg 720
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Mus musculus (strain:C57BL/6J) 10 day old male pancreas CDNA temporary clone_lib:RIKEN full-length enriched mouse CDNA library clone:1810015L03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 tcacgcacgtgctgaacgcggcccacggccgctggaacgtggacactgggcccgactact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accycyacatygacatccaytaccacygcytygayyccyacyacctycccaccttcyacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcagtgtcttcttctaccggoggcagccttcatcgacagagcgttaagcgacgaccaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acctgatgatccacaaggacatgaccctggtggacgccatccagcaagtggccaagaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 ACCTCATGCTGTACCACCACCTTACCCTCGTGGAGGCCATCAAGAAAGTCAAAGACCACC
                                                                                                                                                                                                                                                                                                                                                                   8.
                                                                                                                                                                                                                                                                                                                           Length 990;
                                                                                                                                                                                                                                                                                                                                                                 164; Indels
                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                         Score 176.6; DB 1. Pred. No. 2.8e-22;
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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AK007513.1 GI:12841108
                                                                                                                                                                                                                                                                                                                           15.2%;
64.5%;
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
SE 5 (bases 1 to 1104)
Alzawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
Inotani,K., Ishi,X., Itoh,M., Izawa,M., Kato,H., Kawai,J.,
Miyazaki,T., Hara,A., Hayatau,N., Izawa,M., Kato,H., Kawai,J.,
Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T.,
Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y.,
Okido,T., Owa,C., Saito,H., Saito,H., Sakai,C., Sakai,K., Sano,H.,
Sasaki,D., Shibata,K., Shibata,Y., Shinaqawa,A., Sakai,T.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,
Toshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (10-101-200) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemome: Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-Cho, Tsurumi-Ku, Yokohama,
Kanagawa 239-0045, Japan (E-mail:genome-reseasc-risit-Our Laboratory for Sciences Center (GSC),
Fax:81-45-503-9216)
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                                                                                                                                                                                     2 (bases 1 to 1104)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome research. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (bases 1 to 1104)
The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI;
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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/db_xref="MGD:MGI:1914209"
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1 (bases 1 to 471)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Grasas, E., Wary, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                            CDNA library
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libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
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                                                                                                                                                                      Indels
                                            enriched
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                        DB 12;
                                                                                                                                      Score 166.2; DB 12;
Pred. No. 1.9e-20;
0; Mismatches 153;
                           /tissue_type="pancreas"
/clone_lib="RIKEN full-length
/dev_stage="10 day old"
177 c 350 g 208 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF774179 471 bp mRNA
273763 MARC 3BOV Bos taurus cDNA
BF774179.1 GI:12122079
/clone-"1810015L05"
                                                                                                                                      14.3%;
llarity 63.3%;
Conservative
                /sex-"male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcagctggtgcag 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 TAGGCTGCGGCAG 443
                                                                                                                                                      Similarity
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BF774179
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AUTHORS
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
POR PRIMERS
PORABACKGCTATGACCAT
BACKWARD: AGGAACACCAT
BACKWARD: GTTTCCCAGTCAGGAG
BACKWARD: GTTTCCCAGTCAGGAG
BACKWARD: GTTTTCCAGTCAGAGA
Seq primer: ATTTAGGTGACATATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 415)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
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                                                                                                                                                                                                                                                                    ocoled tissue from marrow, alveolar fetal semitendonosus muscle, and fetal
                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle." 1 to 15 c 160 g 73 t 1 others
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CDNA clone
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9
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Pred. No. 3.2e-20;
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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Bento
                                                                                                                                             Location/Qualifiers
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EST175343 Infant brain,
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A1372800
A1372800.1 GI:4152666
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illarity 65.8%;
Conservative 0
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Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, M.M., Fritchman, J.L., Geoglagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Dimke, D.P., Feor, L.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hudson, P. Hu, J. S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wel, Y., Kosen, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: BA, Mi3-derived; Site_1: HindIII; Site_2: MotIs The infant brain library, constructed by Bento NotI: The infant brain library, constructed by Bento Soares, Columbia University, was oligo-(dT) primed and directionally cloned into an Mi3-derived plasmid using total brain mRNA from a 72-day old human female afflicted with Spinal muscular atrophy." 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395
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14.1%; Score 164; DB 10;
Best Local Similarity 63.3%; Pred. No. 7.1e-20;
Matches 264; Conservative 0; Mismatches 147;
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)
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The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                  Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700022L10, full insert sequence.
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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KEYWORDS
SOURCE
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19 301 c 259 g 229 t
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221. .817
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 Exploration Research Group
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Pred. No. 5.8e-20;
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                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711 aagcagctggtgcagcagaggcgacg 736
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57.7%;
                                                                                                                                                                                                                                                                                      /sex="male"
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                     Chordata, Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

1 148 c 135 g 92 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized
                                                                                                                                                                      5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTB: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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Pred. No. 1.7e-19;
0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
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                                                                                                                                                                        CDNA
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Plate: 42 row: P column: 11
Seq primer: ATTTAGGTGACACTATAG.
                       810
                                                                                                                                               BE751020 456 bp mRNA
202721 MARC 2BOV Bos taurus
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PCR PRimers
BE751020.1 GI:10165012
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chc
Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 13.9%;
Local Similarity 62.7%;
les 269; Conservative
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⁶²¹ atgaccetg 629 | | ||||| 446 CTCTCCCTG 454 δ

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Search completed: February 8, 2002, 19:05:04 Job time: 3059 sec

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(without alignments)
9581.580 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                    930621 segs, 428662619 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	λίσε	Match Length DB ID Description	1262 22 AAD09495	1212 21 AAA75684).7 556 22 AAI41184 Probe #9870 used t	234 22 AAI54224	636 22 AAD09497	1878 22 AAI58512	1691 22 AAI62760	1491 21 AAC61100	1917 22 AAD09496	904 22 AAF63571	
ø	Query	Match Le	94.1	91.9	20.7	20.1	17.5	17.5	17.5	17.4	17.3	17.1	
		Score	1096.6	1071	241	234	204.2	204.2	203.4	202.6	201	199.4	
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	Human CSAPTP-4 ope	Human CSAPTP-4 cod	CDNA sequence enco	Human DSP-7 cDNA.	Human polynucleoti	Human hydrolase-11	Murine phosphatase	Human CSAPTP-2 ope	~		Human phosphatase	Human ORFX ORF2637	Human ORFX ORF683	Human SGP003 part1	Human secreted pro	Human cDNA encodin	Human polynucleot1	Human genomic DNA	Human polynucleot1	Human polynucleoti	Human polynucleot1	MAP-kinase-phospha	Partial MAP kinase	Human lung tumour	Human lung tumour	Human lung tumour	Human lung tumour		_	Probe #5629 for ge	Probe #6054 used t	Probe #14853 for g	Probe #19236 used	Murine TGF-beta bi	
	AAA09032	AAA09031	AA246148	AAC62749	AAI59133	AAC60226	AAF63566	AAA09028	AAA09027	AAD09494	AAQ68661	AAC77082	AAC75128	AAD09503	AAC16446	AAC61101	AA160298	AA162831	AA159134	AA160919	AA160920	AAQ72864	AAQ96010	AAF68858	AAF68877	AAF68878	AAF68856	AAF68859	AAC77082	AA115696	AAI37368	AA124920	AA150550	AAA29063	
	21	21	21	21	22	22	22	21	21	22	15	21	21	22	21	21	22	22	22	22	22	15	16	22	22	22	22	22	21	22	22	22	22	71	
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	197.8	197.8	197.8	197.8	196.2	175	165.2	_:	161.6	145.8	133	133	123	119.4	110	105.6	105.6	103.4	86	96.4	96.4	9.07	9.02	9.02	9.07	9.07	69	69	æ	9	66.4	S	65.2	63.2	
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ALIGNMENTS

Human; SGP003 phosphatase polypeptide; phosphatase-related disease; immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; paln; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematopoletic cancer; mood disorder; cardiant; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neurological disorder; virucide; nootropic; cerebroprotective; therapy; hypotensive; immunosuppressive; antipsoriatic; antipsoriatic; analgesic; hypertensive; antificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome CHR10; ds. Human SGP003 phosphatase polypeptide encoding DNA. AAD09495 standard; DNA; 1262 BP (first entry) 10-SEP-2001 AAD09495; AAD09495 RESULT

sapiens. Homo

/product= "Human SGP003 phosphatase polypeptide" /transl_except= (pos:492..494, aa:Leu) Location/Qualifiers /*tag= a 240..902

WO200146394-A2.

28-JUN-2001

541

482

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The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, and disorders, including cancers of tissues, cancers of netabolic disorders, including cancers of tissues, cancers of nematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, ingraines, pain, disorders, hypotension, uppertension, psychotic disorders, neurological disorders, hypotension, uppertension, psychotic disorders, neurological disorders, hypotension, uppertension, psychotic disorders, neurological disorders, hypotension, dispendension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present sequence is a DNA encoding human SGP003 phosphatase (DSP) and MAPP CHIPIN CH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain or
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99US-0175766.
2000US-0178078.
2000US-0179301.
                            2000WO-US34736
                                                                                                                                                                                                                                                                               Α,
                                                                                                                                                                                                                                                                               Martinez
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                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE04837
                            21-DEC-2000;
                                                                                                                                        25-JAN-2000;
                                                                                                                                                               31-JAN-2000;
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Flanagan P;
                                                                               21-DEC-1999;
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22; Length 1262; T; 0 other; Sequence 1262 BP; 287 A; 356 C; 392 G; 227 94.1%; 98.2%; Query Match Best Local S

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241
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                        Gaps
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                                                                                       gcggccaggccccggcacacccagctgcagaaaggagagaaatcccttggctctaaaat
                                                                                                            goggocaggocacacccagotgcagaaaggagagagaaatcccttggotctaaaat
                                                                                                                                            gacatctggagaagtgaagacaagcctcaagaatgcctactcatctgccaagaggctgtc
                                                                                                                                                                             gccgaagatggaaggaagggaaggaggaggactactgcaccctggagctttgagct
                                                                                                                                                                                                                       ggagcggctcttctggaagggcagtccccagtacacccacgtcaacgaggtctggcccaa
                                                                                                                                                                                                                                 5;
Score 1096.6; DB 22; Lengt
Pred. No. 8.4e-236; 0
0; Mismatches 19; Indels
          Similarity 98.2
20; Conservative
            Best Local Simi
Matches 1120;
                                                                 122
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                                                                                                                                                                                                                                                             781
                                                                                                                                                                                                                                                                                                        841
                                                                                                                                                                                                                                                                                                                             961
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                                                                                                                                                                                                                                                                                                                                                                                                                                         taagatcctggttcactgcgtcatgggccgcagccggtcagccacctggtcctggccta
                                                                                                                                                                                                                            cctggcctaggactccagagaagggatggtgaaaccgaagctcgactcttccaaaaccatc
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                                                                                                                                                taagatcctggttcactgcgtcatgggccgcagccggtcagccacctggtcctggccta
                                                                                                                                                                       cctgatgatccacaaggacatgaccttggtggacgccatccagcaagtggccaagaaccg
                                                                                                                                                                                             cctgatgatccacaaggacatgaccctggtggacgccatccagcaagtggccaagaaccg
                                                                                                                                                                                                                   ctgcgtcctcccgaaccggggcttttgaagcagctccgggaagctggacaagcagctggt
                                                                                                                                                                                                                                                              gcagcagaggcgacggtcccagcgccaggacggtgaggaggaggatggcagggagctgta
                                                                                                                                                                                                                                                                                   gcagcagaggcgacggtcccagcgccaggacggtgaggaggaggatggcagggagctgta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aggagcatgccacgctgcaccaagtctcctgctttggttttgttttttggtgaagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agagggaaaaagatttttaaaatgtgtaggcagtatgttgtgattaaacgtttggctttg
                                                         cogcoacatogacatccagtaccacggogtggaggccgacgacctccaccttcgacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a human regulator of intracellular phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ggaagagggaaaaagatttttaaaatgtgtaggcagtatgttgtgattaaacgtttggct
                       ggagcggctcttctggaagggcagtccccagtacacccacgtcaacgaggtctggcccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1192 ttgtttaaaaacaaaaaaa
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ID AAI411
XX AAI411
AC AAI411
XX I7-OCT
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                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist or antagonists of HRIP polypeptide. HRIP and its agonist or antagonist care useful for treating a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or diagnosed include neurological disorders such as stroke, Parkinson's disease, demyelinating diseases, bacterial and viral meningitis and other developmental disorders of the central nervous system.

The control of the control of the captain of the cancer of the disorders of the captain and other actions actinic keratosis, arteriosclerosis, atherosclerosis and cancer of including leukaemia, melanoma, myeloma and cancer of the adrenal gland, all aldder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases, allergies, bronchitis, diabetes mellitus, including leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 :
                                                                                "regulator of intracellular phosphorylation"
                                                                                                                                                                                                                                                                                                                             Novel human intracellular phosphorylation regulator polypeptides and polynucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geggecaggececeggeacaccagetgeagaaaggagagagaaaateeettggetetaaaat 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gacatctggagaagtgaagacaagcctcaagaatgcctactcatctgccaagaggctgtc 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                       Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1212;
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                                                                                                                                                                                                                                                       Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis, microbial infection and trauma
arthritis; microbial infection; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1071; DB 21;
Pred. No. 4.4e-230;
0; Mismatches 25;
                                                                                                                                                                                                                                                       Hillman JL,
                                            Location/Qualifiers
172..837
/*tag= a
/product= "regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 94; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
91.9%;
Best Local Similarity 97.4%;
Matches 1131; Conservative (
                                                                                                                                                                             99US-0125593.
99US-0135049.
99US-0143188.
                                                                                                                                                                                                                                                       Ξ,
                                                                                                                                                        2000WO-US07277
                                                                                                                                                                                                                                                      Yue
                                                                                                                                                                                                                              (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                   Au-Young J;
                                                                                                                                                                                                                                                                                        WPI; 2000-602121/57.
P-PSDB; AAB18667.
                                                                                                       WO200055332-A2
                       Homo sapiens
                                                                                                                                                                             18-MAR-1999;
20-MAY-1999;
09-JUL-1999;
                                                                                                                                                      17-MAR-2000;
                                                                                                                                21-SEP-2000
rheumatoid
                                                                                                                                                                                                                                                       Bandman O,
                                                                                                                                                                                                                                                                    Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
               Probe #22910 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctgcagaaaggagagaaaatcccttggctctaaaatgacatctggagaagtgaagacaag 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggaggaggactactgcaccctggagcctttgagctggagcggctcttctggaagggcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 tececagtacaceceacgteaacgaggtetggeecaagetetacattggegatga 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                   Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human SGP060 phosphatase polypeptide encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 234 BP; 40 A; 71 C; 58 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.1%; Score 234; DB 22;
100.0%; Pred. No. 2.5e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID No 22910; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0201456.
30-UJN-2000; 2000US-06084.08
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                             ; 2000us-0180312.
; 2000us-0207456.
; 2000us-0608408:
; 2000us-0632366.
; 2000us-0236359.
                                                                                                                                                                                                2001WO-US00663
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Best Local Similarity 100.
Matches 234; Conservative
                                                                    SS.
                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488897/53
                                                                    genetic disorder;
                                                                                                                                 WO200157272-A2
                                                                                                    Homo sapiens
                                                                                                                                                                                                30-JAN-2001;
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                                                                                                                                                                 09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaaggagagaaaatcccttggctctaaaatgacatctggagaagtgaagacaagcctcaa 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
 to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tacatgccccacggaccagaacctcccgacgcggccaggccccggcacacccagctgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggactactgcaccctggagcctttgagctggagcggctcttctggaagggcagtcccca
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human placenta -
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                Probe; microarray; human; placenta; antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 556 BP; 115 A; 153 C; 154 G; 134 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 241; DB 22;
Pred. No. 8.6e-45;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID No 9870; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                         26-MAY-2000; 20000S-0207456.
30-JUN-2000; 2000US-0608408.
21-SEP-2000; 2000US-06334687.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023659.
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                                                                                                                                                                             30-JAN-2001; 2001WO-US00663
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Best Local Similarity 89.6
Matches 259; Conservative
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                                                 genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
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Probe #9870 used
                                                                                                              WO200157272-A2
                                                                                 Homo sapiens
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AC AA1542
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152 433 212

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immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematopoietic cancer; mood disorder; cardiant; parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiavascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neurological disorder; virucide; nootropic; cerebroprotective; therapy; hypotensive; manuosuppressive; antipsoriatic; antiasthmatic; antistingal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MKP; migraine; chromosome 8pll.1-q11.1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
                                                                                                                                                                                                                                 /*tag= a
/product= "Human SGP060 phosphatase polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manning G,
phosphatase polypeptide;
                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 29; Fig 1; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                      21-DEC-1999; 99US-0173255.
28-DEC-1999; 99US-0175766.
25-JAN-2000; 2000US-0178078.
31-JAN-2000; 2000US-0179301.
                                                                                                                                                                                                                                                                                                                            21-DEC-2000; 2000WO-US34736.
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P-PSDB; AAE04839.
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                                                                                                                                                                           sapiens
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Sudarsanam

The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of hematopoletic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection The present sequence is a DNA encoding human SCP006 phosphatase (DSP) and MAP and MAP and MAP SCP060 gene maps to chromosomal position

Sequence 636 BP; 123 A; 207 C; 182 G; 124 T; 0 other;

17.5%; 64.8%;

Matches 321; Conservative

Similarity

Query Match Local

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Score 204.2; DB 22; Length 636;
Pred. No. 1.5e-36;
0; Mismatches 168; Indels 6;
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Gaps

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                  307 cccgaggcctatgaggggctgggcatccgctacctgggtgttgaggcccacgactcgcca
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                                                             351 aaggeggggtteacgeacgtgetgaacgeggeecaeggeeggtggaacgtggg
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Yang Y,
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Wehrman T,
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2000US-0552317.
2000US-0598042.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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Vang Z,
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09-JUL-2000;
19-JUL-2000;
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Wang J,
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AAI62760 standard; cDNA; 1691

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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huttington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                   the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                 to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                      Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1878 BP; 417 A; 546 C; 560 G; 355 T; 0 other;
  Drmanac RT;
                                                                                                                                                                                             Claim 1; SEQ ID NO 715; 10078pp; English
  Goodrich R,
                                                                                                                                                                                                                                                 The invention relates
                                                WPI; 2001-442253/47.
P-PSDB; AAM39356.
  Zhou P,
  OA,
  zhao
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ï Gaps Score 204.2; DB 22; Length 1878; Pred. No. 2e-36; 9 Indels 168; 0; Mismatches 17.5%; 64.8%; Conservative Similarity 321; Query Match Local Matches

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651 gccaagaaccgctgcgtcctcccgaaccgggctttttgaagcagctccgggagctggac 710
| 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 1111 || 
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gcetttgagetggageggetettetggaagggeagtececagtacaeceaegteaacgag 290
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                                                                                                                      682 gtcttcgagttggagcggctcctctacacaggcaagacagcctgtaaccatgccgacgag 741
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1156 cgcaggctgcggcag 1170

RESULT 7 AAI62760/C

711 aagcagctggtgcag

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immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM42347-AAM42415) useful for preventing, treating or ameliaring medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 19; 532pp + Sequence Listing; English
                                                                                               Human; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
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                                              (first entry)
                                                                       Human cDNA SEQ ID NO 19.
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P-PSDB; AAM42355.
                                                                                                                                                                                                                                 WO200155449-A1
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                           07-JUL-2000;
14-JUL-2000;
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25-SEP-2000;
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2000WO-US09321

07-APR-2000;

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WO200060100-A1 Homo sapiens.

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             In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastroofitestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTGGCCAGGCCTCTATCTCGGAGACCAGGACATGGCTAACAACCGCCGGGAGCTTCGC 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                       1206 GTCTTCGAGTTGGAGCGGCTCCTCTACACAGGCAAGACAGCCTGTAACCATGCCGACGAG 1147
                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtctggcccaagctctacattggcgatgaggcgacggctggaccgctataggctgcag 350
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   nucleic acids, proteins, antibodies and (ant)agonists are useful
                                                                                                                                                                                                                                                                                                                                  Score 203.4; DB 22; Length 1691;
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                                                                                                                                                                                                                                                                           Sequence 1691 BP; 320 A; 512 C; 480 G; 375 T; 4 other;
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2; Mismatches 168;
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                                                                                                                                                                epilepsy; and (f) infectionand parasitic infections.
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Matches 319; Conservative
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Best Local S
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This invention relates to an isolated dual specificity phosphatase-9 (DSP-9) and its variant. The DSP-9 protein has the ability to dephosphorylate an activated mitogen activated protein (MAP) kinase. Included in the invention are an expression vector comprising a polynucleotide encoding the DSP-9 protein, a host cell transformed by the expression vector, and an antibody that specifically binds to DSP-9. DSP-9 has cytostatic; immunosuppressive; antiallergic; and antiproliferative activity. DSP-9 modulating agents are useful for modulating a proliferative response, differentiation or survival of cell which displays contexting inhibition of cell growth, anchorage independent growth or an altered intercellular adhesion property, in a patient. DSP-9 agonists and antagonists are also useful for treating a disorder associated with DSP-9 activity such as Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune disease, albormal cell growth, abnormal cell prowth, abnormal cell proliferation and cell cycle abnormalities. The present sequence
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                                                                                                                                                                                                                                                                                            Dual specificity phosphatase-9 which dephosphorylates activated mitogen-activated protein kinase, used to identify agents that inhibit DSP-9 activity and modulate cell proliferation, differentiation, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
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Pred. No. 4.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents human cDNA encoding DSP-9.
                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 1; 66pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; tranquilliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypotrensive; antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; MRP; migraine; chromosome idqq13.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase polypeptide is used to treat immune-related diseases and disorders,
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                                                                     709 aaagaccaccgaggcatcatccccaaccggggcttcctgaggcagctcctggccctggac 768
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gtcctggcctacctgatgatccacaaggacatgacctggtggacgccatccagcaagtg
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/product= "Human SGP014 phosphatase polypeptide"
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Immune-related diseases and disorders, cardiovascular disease, 
neuronal-associated diseases and metabolic disorders
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990S-0175766.
2000US-0178078.
2000US-0179301.
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P-PSDB; AAE04838.
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cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders, including cancers of tissues, cancers of haematopoietic origin, diseases of central and peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, diabetes, migraines, partins, bacteria, and fungi, ocular diseases, diabetes, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present sequence is a DNA encoding human SCPO14 phosphatase polypeptide. This sequence is classified as dual specificity phosphatase (DSP) and MAP kinase phosphatase (MKP). SGP014 gene maps to chromosomal position
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The present invention relates to phosphatase proteins and coding. Sequences. The present sequence is one such phosphatase coding sequence. Phosphatases are enzymes that catalyse the dephosphortation of proteins modified by phosphorylation of serine, threonine or tyrosine residues. The phosphatases are useful for treating a variety of diseases: for example cancer e.g. breast, urogenital, prostate, head, neck, lung cancers, synovial sarcomas, renal cell carcinoma, non-small cell lung cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach parhophysiological hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, Pepillon-Lefevre syndrome, Cowden disease, ectodermal dysplasia, Moeblus syndrome, blornsted syndrome, Bannayan Zonana syndrome, schizophrenia and
                                                                                                                                                                                                                                                                                                     New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders
                                                                                                                                                                                                                       Lioubin M;
                                                                                                                                                                                                                     Flanagan P,
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P-PSDB; AAB73219.
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                 Homo sapiens.
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Query Match 17.1%; Score 199.4; DB 22; Length 904; Best Local Similarity 64.3%; Pred. No. 1.9e-35; Matches 299; Conservative 0; Mismatches 166; Indels 0;
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AAC76543 standard; cDNA; 1200

08-FEB-2001

AAC76543;

antianaemic, gene therapy; carcer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID, AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss. Human; open reading frame; ORPX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyrold; Human ORFX ORF2098 polynucleotide sequence SEQ ID NO:4195

31-MAR-2000; 2000WO-US08621. WO200058473-A2. 05-OCT-2000

sapiens.

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99US-0127607. 99US-0127636. 99US-0127728. 2000US-0540763. 31-MAR-1999; 02-APR-1999; 05-APR-1999; 30-MAR-2000;

Sequence 904 BP; 183 A; 282 C; 249 G; 190 T; 0 other;

Ξ (CURA-) CURAGEN CORP. Shimkets RA,

WPI; 2000-602362/57. P-PSDB; AAB42334. Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 5; Page 3391-3392; 5507pp; English.

antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifungal; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy exctors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive;

New cardiovascular system associated protein tyrosine phosphatases are used in the diagnosis and treatment of e.g. immune disorders, anti-proliferative disorders, metabolic disorders and cardiovascular

disorders

2000-293136/25 P-PSDB; AAY92177

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erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                                                              17.1%; Score 199.4; DB 21; Length 1200; 64.3%; Pred. No. 2.1e-35;
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                                                                                                                                      166;
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30-SEP-1998;
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This sequence encodes a cardiovascular system associated protein tyrosine phosphatase 4 (CSAPTP). The CSAPTP nucleic acid and protein molecules are used to modulate regulation of cellular processes. CSAPTP nucleic acid and protein molecules and modulators of CSAPTP activity and cacid and protein molecules and modulators of CSAPTP activity and cacid and protein molecules and modulators of CSAPTP activity and disorder characterized by aberrant CSAPTP expression or activity. These disorder characterized of immune disorder, an anti-proliferative disorder, a proliferative disorder e.g. renal and lung carcinomas, a metabolic disorder e.g. disorder e.g. renal and lung carcinomas, a metabolic disorder rising cidabetes, viral pathogenesis, a neural disorder, a cardiovascular disorder phosphorylation of a phosphorylated protein. Anti-CSAPTP containing and recombinantly produced CSAPTP carlitate the purification of a phosphorylated protein in cell supernatant for evaluating from cells, to detect CSAPTP protein in cell supernatant for evaluating the level of CSAPTP expression and to monitor protein levels in tissue as procedure. CSAPTP nucleic acids, antibodies and protein molecules can be used in screening assays and in predictive medicine e.g. prognostic assays, monitoring clinical trials and pharmacogenetics.
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Pred. No. 4e-35;
0; Mismatches 167;
                                                                                                                                                                  Claim 1; Page 155-156; 156pp; English
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al Similarity 64.1%;
298; Conservative (
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cgctataggctgcagaaggcggggttcacgcacgtgctgaacgcggcccacggccgctgg 395 aagagcaagctgatccagctgggaatcacccacgttgtgaatgccgctgcaggcaagttc 318

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This sequence encodes a cardiovascular system associated protein tyrosine phosphatase 4 (CSAPTP). The CSAPTP nucleic acid and protein molecules are used to modulate requiation of cellular processes. CSAPTP nucleic acid and protein molecules and modulators of CSAPTP activity and expression can be used to treat a subject with a disorder characterized by aberrant CSAPTP expression or activity. These disorder characterized an immune disorder, an anti-proliferative disorder, a proliferative can immune disorder e.g. an immune disorder, an anti-proliferative disorder, a cardiovascular cisones, viral pathopanesis, a neural disorder, a cardiovascular cisones, viral pathopanesis, a neural disorder, a cardiovascular cisones, viral maproper phosphorylation of a phosphorylated protein. Anti-CSAPTP con improper phosphorylation of a phosphorylated protein. Anti-CSAPTP continued to disorder rising from cells, to detect CSAPTP protein in cell supernatant for evaluating content of a clinical testing procedure to determine efficacy of a treatment procedure. CSAPTP nucleic acids, antibodies and protein molecules can be procedure. CSAPTP nucleic acids, antibodies and protein molecules can be used in screening assays and in predictive medicine eg, prognostic measure monitorylar or acid nucleic acids and pharmaconemics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cardiovascular system associated protein tyrosine phosphatases are used in the diagnosis and treatment of e.g. immune disorders, anti-proliferative disorders, metabolic disorders and cardiovascular
                                                                                                                                                                                                                                                                                                                                        Cardiovascular system associated protein tyrosine phosphatase 4, CSAPTP-4; cytostatic; immunomodulatory; antidiabetic; virucide; hypotensive; cardiant; tyrosine phosphatase modulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assays, monitoring clinical trials and pharmacogenetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 153-154; 156pp; English.
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1..663
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/product= CSAPTP-4
                                                                                                                                                                                                                                                                  Human CSAPTP-4 coding sequence.
                                      AAA09031 standard; DNA; 928 BP
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98US-0164193.
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P-PSDB; AAY92177.
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30-SEP-1998;
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Azimzai Y;
          gccatccagcaagtggccaagaaccgctgcgtcctcccgaaccggggctttttgaagcag 695
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                                                       379 goggacgacaaccccttcttcgacctcagtgtctactttctgcctgttgctcgatacatc 438
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H, Azimzai
                                     gccgacgacctgcccaccttcgacctcagtgtcttcttctacccggcggcagccttcatc
aacgiggacactgggcccgactactaccgcgacatggacatccagtaccacggcgtggag
                                                                                                                                                                                                                                                                                                                     cDNA sequence encoding a human phosphorylation effector PHSP-11.
                                                                                                                                                                                                                                                                                                                                       Human; phosphorylation effector; PHSP; proliferative disorder;
immune disorder; neuronal disorder; ss.
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Au-Young J, Gorgone GA, Yue
                                                                                                                                                                                          696 ctccgggagctggacaagcagctggtgcagcagaggcgacggtcc 740
                                                                                                                                                                                                     Location/Qualifiers
28.774
74.tag — //Product - "phosphorylation effector"
                                                                                                                                                                                                                                                            AAZ46148 standard; cDNA; 1023 BP.
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98US-0173482.
98US-0106089.
98US-01093.
99US-0113796.
99US-0173482.
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Reddy R, Lu DAM, Shih LL;
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P-PSDB; AAY68779.
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03-NOV-1998
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Score 197.8; DB 21; Length 928; Pred. No. 4.4e-35; 0; Mismatches 167; Indels 0;

Query Match
Best Local Similarity 64.1%;
Matches 298; Conservative (

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treatment
                                                                                                               AA246138-246168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP
                                         prevention of proliferative, immune and neuronal disorders
                      diagnosis,
                      useful for the
                    phosphorylation effectors
                                                                              Page 125; 142pp; English.
                      human
                                                                              Claim 9;
                    New
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Sequence 1023 BP; 219 A; 295 C; 299 G; 210 T; 0 other;

antagonists are useful for treating or preventing disorders associated with increased PHSP expression/activity.

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Sequence 1300 BP; 266 A; 398 C; 374 G; 262 T; 0 other;

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Mitogen-activated protein kinase; MAP kinase; dual-specificity phosphatase; DSP-7; cytostatic; immunosuppressive; antiallergic; apoptosis modulation; gene expression modulation; Duchenne muscular dystrophy; cancer; graft-versus-host disease; autoimmune diseases; allergy; metabolic disease; ss.
                            BP.
                          AAC62749 standard; cDNA; 1300
                                                                                                                   Human DSP-7 cDNA.
                                                                                    05-FEB-2001
                                                        AAC62749
              AAC62749
RESULT
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The present sequence is given in a method relating to the phosphatean sequence is given in a method relating to the phosphatease DSP-7. The antibody specific to DSP-7 and the antisense polynucleotide of the nucleic acid encoding DSP-7 are useful for detecting DSP-7 expression in a sample which comprises an RNA or cDNA preparation. The antibody is linked to a support material and a detectable marker and the amount of DSP-7 polynucleotide hybridisation assay. The isolated DSP-7 polynucleotide is determined using PCR or hybridisation assay. The isolated DSP-7 polynucleotide is useful for screening agents that modulate DSP-7 activity. The identified agents are useful for treating Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities.
                                                                                                                                                                                                                                                                                                                      Novel dual-specificity mitogen-activated protein kinase phosphatase polypeptide used in assays to identify agents that modulate the enzyme's activity, which are useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 1; 70pp; English
                                                                                                         2000WO-US09257
                                                                                                                                             99US-0128207
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                                WO200060098-A1
Homo sapiens
                                                                                                         07-APR-2000;
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                                                                    12-OCT-2000
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human.*
sp_invertebrate:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_mhc:* sp_organelle:* sp_phage:* sp_rodent:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9qv17 mus musculu	Q9uii6 homo sapien	Q9da25 mus musculu		Q9d700 mus musculu	Q9vwn2 drosophila	Q9d7x3 mus musculu	Q9btw0 homo sapien	Q9nrw4 homo sapien	044128 caenorhabdi	Q9zr37 arabidopsis	Q9luq6 arabidopsis	Q9ffa8 arabidopsis	Q99n11 mus musculu	Q9m8k7 arabidopsis	Q99kc2 mus musculu	Q9nky1 drosophila	O9nsw1 homo sapien	_	·.
ID	090x37	911060	09DA25	Q9BV47	002060	Q9VWN2	Q9D7x3	Q9BTW0	Q9NRW4	044128	Q92R37	95U160	Q9FFA8	099N11	Q9M8K7	Q99KC2	Q9NKY1	Q9NSW1	013524	
80	17	4	1	4	11	ស	11	4	4	S	10	10	10	11	10	11	S	4	4	
% Query Match Length DB	198.	198	198	211	198	245	185	98	184	365	198	198	946	184	167	436	1045	303	394	
& Query Match	39.7	39.7	39.2	38.3	37.9	29.8	28.9	20.1	17.7	17.6	17.5	17.5	17.4	17.2	17.2	16.6	16.6	16.6	16.6	
Score	461	460.5	455	445	440	345.5	335	233	205	204.5	203.5	203.5	201.5	200	199.5	193	193	192.5	192.5	
Result No.	П	7	Э	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	

Score 461; DB 11; Length 198; Pred. No. 5.4e-36;

39.78;

Query Match Best Local Similarity

Q13649 homo sapten Q9aty4 zea mays (m Q9c5s1 arabidopsis Q9v180 drosophila Q91790 xenopus lae Q91790 xenopus lae Q95984 homo sapten Q9c033 homo sapten Q4253 qallus gall Q9y6v6 homo sapten Q95147 homo sapten Q4253 qallus gall Q9y6v6 homo sapten Q90606 mus musculu Q99n12 mus musculu Q90vhv8 drosophila Q9cxy9 mus musculu Q9cs15 mus musculu Q9cs15 mus musculu Q9cs15 mus musculu Q9d715 mus musculu	PRT; 198 AA. eated) st sequence update) st annotation update) IFICITY PHOSPHATASE TS-DSP6). Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. E. M., Haneji T., Kikuchi K.; erization of a novel dual specificity nvolved in spermatogenesis."; idual specificity phosphatase."; idual specificity phosphatase."; atase. ASE_1: 1. ASE_2: 1.
Q13649 Q9ATY4 Q9CSS1 Q9VU80 Q91790 Q9BY84 Q9C0G3 Q95147 Q9C0G3 Q9D6F6 Q9D6F6 Q9D6F6 Q9D6F6 Q9DCF8 Q9VW8 Q9CXP9 Q9CYW4 Q9C	INARY; PRT; 198 AA. Lrel. 13, Created) Lrel. 13, Last sequence update) Lrel. 17, Last annotation update E (DUAL-SPECIFICITY PHOSPHATASE e). Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Murida and characterization of a nove possibly involved in spermatogenerate possibly involved in spermatogenessibly involved involv
000014441111111111111111111111111111111	;; 13, C 13, L 17, L 17, L 17, L 17, L 17, L 17, L 10, L 10, L 10, L 10, L 11,
4111 6611 6613 6613 6613 6613 6613 6613	PRELIMINARY; (TrEMBLrel. 13, C (TrEMBLrel. 13, I (TrEMBLrel. 17, I PHATASE (DUAL-SPI (MOUSE). etazoa; Chordata, theria; Rodentia, 0090; M NA. 3896, PubMed-1056 Shima H. Watana, 100109 and chara phatase possibly 344:819-825(1999) 344:819-825(1999) 345:0000 to the i 100100 of a novel 1100100 of a novel 20; BAA89411.1; 20; BAA89411.1; 20; BAA89411.1; 20; BAR15037.1; 20; BAR1504.1; 20; BAR17R_PHOSPH 0056; TYR_PHOSPH
	PRELIMIN 000 (TrEMBLE 001 (TrEMBLE 1001 (TREMBLE 1102 (Mouse) 1102 (Mouse) 12 Metazoa; 13 Metazoa; 14 Metazoa; 15 Metazoa; 16 Eutheria; 17 Cloning and 18 A : 819- 19 A : 819- 10 A : 819-
192.5 180 181 182 181.5 170 170 170 174 173 173 173 173 173 173 173 173 173 173	1 1007J7 007J7 1-MAY-27
01000000000000000000000000000000000000	RESULT OOG ON THE PROPERTY OF
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Query Match 39.2%
Best Local Similarity 49.2%
Matches 93; Conservative
             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 AA;
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---RRETGR 197
                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
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                                                              81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
                                                                            81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
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                     PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                               12 PKIHGAVQVSPYQPPTLASLQRLLWVRRTATLTHINEVWPNLFLGDAYAARDKGRLIQLG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 PKMEEEGEEEDYCTPGAFELERLFW-KGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAG 80
                                                                                                                                                                                                                                                                                                                                                                      Nakamura K., Shima H., Watanabe M., Haneji T., Kikuchi K.;
"Molecular cloning and characterization of a novel dual-specificity
protein phosphatase possibly involved in spermatogenesis.";
EMBL, AB027004; BAA89412.1;
HSSP; P51452; DVHR.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 PKIHGAVQASPYQPPTLASLQRLLWVRQAATLNHIDEVWPSLFLGDAYAARDKSKLIQLG 71
                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                          141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 SKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAJQQVAKNRCVLPNRGFLKQLRELDKQL
  4
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 59; Indels
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Last annotation update)
                                                                                                                                                                                                                                198 AA
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00195, DSPc; 1.
PROSITE; PS00381; TYR_PHOSPHATASE_1; 1.
PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                      Created)
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MEDLINE-20053896; PubMed-10585869;
 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22148 MW;
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 Conservative
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Best Local Similarity
Matches 91; Conserv
                                                                                                                                                     201 VQQRRRSQR 209
                                                                                                                                                                          ---RRETGR 197
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94;
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Arakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Radai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Radai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rabako J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Radota R., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Rodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rayshiawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Anyashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 FTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDH 140
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                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 198
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                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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49.2%; Pred. No. 2e-35;
tive 32; Mismatches 6
198 AA
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SMART; SM00012; PTPC_DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
                                                              (TrEMBLrel. 17, Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
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                                                                                                                                                                     DUAL SPECIFICITY PHOSPHATASE 13.
DUSP13.
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EMBL; AK006247; BAB24480.1; -.
MGD; MGI:1351599; Dusp13.
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RESULT

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AK009781; BAB26501.1;
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                                                                                                                                      Hydrolase.
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KRAIJ-C57BL/65; TISSUE-TONGUE;

KRAMI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawal J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Anata J., Shinaqawa A., Shibata K., Kiyosawa H., Adachi J., Fukuda S., Alto T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Saito R., Saito T., Cokazaki Y., Gojobori T., Bono H., Kasikawa T., Saito R., Ashourer M., Batalov S., Casavant T., Radca K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radca K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radca K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomitan M., Wagner L., Washio T., Sakai K., Okido T., Fullon M., Anno H., Baldarelli R., Barsh G., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Adustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw Bolts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                  46 FELERLLYTGKTACNHADEVWPGLYLGDQDMANNRRELRRLGITHVLNASHSRWR--GTP
                                                              UNKNOWN (PROTEIN FOR MGC:1136).

Mono sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP
                                                                                                                                                                                                                                                                                                                                                                       DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                          Query Match 38.3%; Score 445; DB 4; Length 211; Best Local Similarity 54.3%; Pred. No. 1.9e-34; Matches 89; Conservative 26; Mismatches 47; Indels
                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001613; AAH01613.1; -.
SEQUENCE 211 AA; 23945 MW; 60E944304905086D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          164 LAYLMLYHLILVEAIKKVKDHRGIIPNRGFLRQLLALDRRLRQ 207
                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
211, AA
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PRT;
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PRELIMINARY;
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                                                                                                                                                                TISSUE-LUNG CARCINOMA;
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SEQUENCE FROM N.A.
                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                        NCBI_TaxID=9606;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R.A. Barlew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottler P.,
R.A. Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
R.A. Borkova D., Botchan W.R., Butler H., Cadieu E., Center A., Chandra I.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
R.A. Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R.D. Godson K., Gody F., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,
R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
Alalali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R.A. Mattei B., McIntosh T.C., McLeod M.P., Mopherson D.,
R.A. Martei B., McIntosh T.C., McLeod W.P., Mopherson D.,
R.A. Merkulov G., Milshina N.V., Mobarry C., Morris J., Morpherson D.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 FELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FELERLLYTGKTACNHADEVWPGLYLGDQDMANNRRELRRLGITHVLNASHNRWR--GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                               198 AA; 22419 MW; 11F0CAF4B5620F0E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
37.9%; Score 440; DB 11;
Best Local Similarity 54.3%; Pred. No. 5.3e-34;
Matches 89; Conservative 24; Mismatches 49;
                                                                                                                  pfam; pr00782; DSPC; 1.
SMART; SM00195; DSPC; 1.
SMART; SM0012; prPc_DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                 InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
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MGD; MGI:1914209; 2310043K02Rik
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SEQUENCE FROM N.A.
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                                                                                                          Hayashizaki Y.;
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    A Molton S.M., Moy M., Nurpny B., Murpny L., Muzny D.L.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Ra Nelson D.R., Pettman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Miliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

RA Miliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

RA John Y. R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu X., Smith H.O.,

RA John Y. R., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA John Y. R. Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:185-2195(2000)

R RHSSP, P51452: 1VHR.

FLYBase; FBAN0039076; CG7378.

InterPro: IPR000440; DS_phosphatase.

BR RRT; SM00195; DSPC; 1.

SNART; SM00195; DSPC; 1.

BR PROSITE; PSS0056; TYR_PHOSPHATASE_DUAL; 1.

SROUENCE 245 AA: 27743 MW; E8173DEE878478E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S., Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kledhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    56 NEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHG-RW-NVDTGPDYYRDM-DIQYHGVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 ---KILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDK 198
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 345.5; DB 5; Length 245; 45.1%; Pred. No. 6.4e-25; ive 21; Mismatches 42; Indels 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
S.M., Moy M., Murphy B., Murphy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=STOMACH; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TIEMBLEE]. 17, 01-JUN-2001 (TIEMBLEE]. 17, 101-JUN-2001 (TIEMBLEE]. 17, 1221001500381K. PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 45.19
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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236 EL 237
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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Maasinma J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Sibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 VDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGR--WN 93
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
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RMBL; AKO0874; BAB25864.1; -

MGD; MGI:191599; 2210015003Rik.

InterPro; IPR000340; DS_phosphatase.

InterPro; IPR00037; TYR_phosphatase.

R Pfan; PF00782; DSPC; 1.

SMART; SM0019; PTPC_DSPC; 1.

R PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.

R PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.

SEQUENCE 185 AA; 20472 MW; 62E519E41BE575D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003115.1; -
SEQUENCE 86 AA: 9652 MW; 4DD29AFD5989528B CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (FROTEIN FOR MGC: 2627).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

28.9%; Score 335; DB 11;
Best Local Similarity 43.5%; Pred. No. 4.4e-24;
Matches 74; Conservative 33; Mismatches 57;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 SVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAK-N 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 TKFFPEAISFIDDARRND-SACLVHCLAGISRSVIICLAYLMKTEMCTLDSAYEWVQKRN 301
  Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownker Smaldon N., Snith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vauddin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-99155801; PubMed-10036776;
Gupta R., Huang Y., Kleber J., Luan S.;
Ildentification of a dual-specificity protein phosphatase that inactivates a MAP kinase from Arabidopsis.";
Plant J. 16:581-589(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 365;
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                                                                                                                                                                                                                                    Geisel C., Wamsley P.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ databases
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PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SEQUENCE 365 AA; 41101 MW; 1E416C0E9693AF66 CRC64;
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Last annotation update)
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38.6%; Pred. No. 2.5e-11;
tive 24; Mismatches 55
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InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
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J., Percy C., Rifken L.,
N., Smith A., Sonnhammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 RCVLPNRGFLKQLRELDKQL 200
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                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1997) to the EMBL, AF036685, AAB88308.1; HSSP, Q16828; 1MKP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Les 54; Conserv
                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=BRISTOL N2; Geisel C., Wamsley
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
Submitted (DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                       elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09ZR37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q92R37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gupta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        092R37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 VNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDM--DIQYHGVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 ADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLÀYLMIHKDMTLVD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 AADSPSQNLTRHFKESIKFIHECRLRGES-CLVHCLAGVSRSVTLVIAYYTWTVTDFGWED 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTRAIN-BRISTOL N2;
MEDLINE-9150718; PubMed-7906398;
Wilson R., Anderson K., Baynes C., Berks M.,
Wilson R., Austrough R., Anderson K., Baynes C., Berks M.,
Consel M., Connell M., Copsey T., Cooper J., Coulson A.,
Garton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Garton M., Dear S., Du Z., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Gu J., Huang O., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou
Tu Y., Gu W., Fu G., Huang C.;
"Novel genes expressed in hematopoietic stem/progenitor cells
Myelodysplastic Syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF165519; AAF86649.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 AIQQVAKNR-CVLPNRGFLKQLRELDKQLVQQRRR-----SQRQDGEE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 17.7%; Score 205; DB 4; Length 184; Best Local Similarity 35.7%; Pred. No. 9.3e-12; Matches 61; Conservative 22; Mismatches 66; Indels 3
                                                                                                                                                                                                                                                        Homo sapiens (Human).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo-
NCBI_TaxID=9606;
            5. 概念:
                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHARASE X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20910 MW: B3F962A087C2BA20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00782; DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COSB10.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C05B10.1
                                                                                                                    09NRW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             044128
                                                                                            O9NRW4
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044128
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Q9NRW4
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105 KEDTNLEMYFDECVDFIDEAKRQGGS-VLVHCFVGKSRSVTIVVAYLMKKHGMTLAQALQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 LDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSIYTLQHLGITHVLCLCAN--EIGQSDTQYPDL-FEYQNFSITDDEDSNIESIFQEALD 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAK-NRCVLPNRGF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequenc features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- VWPKLYIGDEATA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50056; TTR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TTR_PHOSPHATASE_LOL; 1.
PROSITE; PS00142; ZINC_PROFFASE; UNKNOWN 1.
SEQUENCE 946 AA; 106195 MW; 39D6967COAC6FED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnolliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO DSPTP1 PROPEIN.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                      A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4%; Score 201.5;
32.6%; Pred. No. 1.7e
iive 24; Mismatches
                                                                                                                                                                                                                                                                                   946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000187; TYR_phosphatase.
InterPro; IPR000180; Zn_f-C2H2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00782; DSPc; 1.
SNART; SM00192; DSPc, 1.
SNART; SM00195; ZnF_CAH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGEEEDYCTPGAFELERLFWKGSPQYTHVNE---
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                                                                                   176 QVAKNRCVL-PNRGFLKQLRELDKQL 200
                                                                                                                        164 HVKSKRPVASPNAGFIRQLQDLEKSM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as. 4:215-230(1997).
AB005244; BAB10045.1; -.
AB025633; BAB10045.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-COLUMBIA; MEDLINE-97471969; Pubmed-9330910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 1 111:
853 ARILINLDKK 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 LKQLRELDKQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99N11
Q99N11;
                                                                                                                                                                                                                                                                                Q9FFA8
                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131
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                                                                                                                                                                                                                          RESULT
09FFA8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
DUAL-SPECIFICITY PROFEIN PHOSPHATASE-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
BUKaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 KEDTNLEMYFDECVDFIDEAKRQGGS-VLVHCFVGKSRSVTIVVAYLMKKHGMTLAQALQ 163
                                                                                                                                                                                                                                                                                                                                                                                       LYIGDEATALDRYRLQKAGFTHVLNA-----AHGRWNVDTGPDYYRDMDIQYHGVEADD 115
                                                                                                                                                                                                                                                                                                                                                                                                                             116 LPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYIGDEATALDRYRLQKAGFTHVLNA-----AHGRWNVDTGPDYYRDMDIQYHGVEADD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 LYLGSVAAASNKNVLKSYNVTHILTVASSLRPAH------PD-----DFVYKVVRVD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 LPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s:
                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.5%; Score 203.5; DB 10; Length 198; 37.0%; Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tabata
                                                                                                                                                                                                                                                                          17.5%; Score 203.5; DB 10; Length 37.0%; Pred. No. 1.4e-11; ive 20; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE ......
STRAIN-COLUMBIA;
Sato. S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA RES. 7:131-135(2000).

EMBL; AB023036; BAB02780.1; -.

EMBL; AB023036; BAB02780.1; -.

InterPro; IPR0000340; DS_phosphatase.

Ffam; PF00782; DSPC; 1.

SNART; SM01195; DSPC; 1.

PROSITE; PS50096; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50096; TYR_PHOSPHATASE_DOAL; 1.

SEQUENCE 198 AA; 22113 MW; 815BBCBE3BFB696A CRC64;
                                                                                                                              PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SEQUENCE 198 AA; 22017 MW; EBFIC98A177E6450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 AA
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HSSP; Q16828; 1MKP.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 QVAKNRCVL-PNRGFLKQLRELDKQL 200
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                                                                                                                                                                                                                                                                                                                                 54; Conservative
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les 54; Conserv
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115 DLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAI 174
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
AOyama K., Matsuda T., Aoki N.;
Aoyama K., Matsuda T., Aoki N.;
"Molecular cloning of a novel dual specificity phosphatase TS-DSP2.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF237619; AAK15038.1; -.
SEQUENCE 184 AA; 20997 MW; 64953325E88AB577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 VNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDM--DIQYHGVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 ADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 VNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEAD 114
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"Arabidopsis thaliana chromosome III BAC F28L1 genomic sequence.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC018907; AAF30304.1;
                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 AIQOVAKNR-CVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEEDGRE 219
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PROSITE; PSS0054; TYR_PHOSPHATASE_DUAL; 1.
SEQUENCE 167 AA: 18431 MW; 57D722910B79A900 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) .
DUAL SPECIFICITY PHOSPHATASE TS-DSP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE DUAL-SPECIFICITY PROTEIN PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.2%; Score 200; DB 11;
33.9%; Pred. No. 2.8e-11;
ative 27; Mismatches 70;
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InterPro; IPR000387; TYR_phosphatase
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(TrEMBLrel. 15, I
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Matches 57; Conservative
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SMART; SM00195; DSPc; 1
                                                                                                     musculus (Mouse).
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STRAIN-CV. COLUMBIA;
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Matches 53; Conserv
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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OM protein - protein search, using sw model
                                              Run on:
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; Search time 12.75 Seconds
(without alignments)
388.292 Million cell updates/sec 8, 2002, 15:44:11 February

220 1 MTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220 US-09-847-519A-2 Perfect score: Sednence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

212252 seqs, 22503292 residues

Word size :

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Issued_Patents_AA:* Database :

/cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1 12 5.5 207 4 US-09-013-881-4 Sequence 4, Appli 2 12 5.5 263 4 US-09-164-193-5 Sequence 5, Appli
ID	207 4 US-09-013-881-4 263 4 US-09-164-193-5
DB	44
Length	207
Query Match Length DB ID	ο. ο.σ.
sult No. Score	12
Result No.	2

ALIGNMENTS

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APPLICANT: Lal, Preet APPLICANT: Lal, Preet APPLICANT: Hilman, Jennifer L. APPLICANT: Gorley, Neil C. APPLICANT: Guegler, Karl J. TILE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                          IE: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
US-09-013-881-4; Sequence: 4, Application US/09013881; Patent No. 6132964
                                                       GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                  Palo Alto
                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
                                                                                                                                                                                                                                                                                                   STATE: CA
                                                                                                                                                                                                                                                                                                                   COUNTRY:
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MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARR: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILLIG DATE: HEREWITH
                                                                                                                                                                                                                                                                                               PF-0470 US
                                                                                                                                                                                               APPLICATE
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Gaps ö Length 207; Score 12; DB 4; Ler Pred. No. 0.00039; Conservative Query Match Best Local Similarity Matches 12; Conserva

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153 SRSATLVLAYLM 164 152 SRSATLVLAYLM 163 ୍ଦ a

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APPLICANT: Acton, Susan L.
TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amerite Reference: MNI-051
CURRENT APPLICATION NUMBER: US/09/164,193C
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                      Length 263;
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Pred. No. 0.00048;
0; Mismatches 0;
RESULT 2
US-09-164-193-5
'S Sequence 5, Application U$/09164193C
'Patent No. 6228582
                                                                                                                                                                                                                                                                                                                                                        5.5%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-164-193-5
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Matches 12; Conserv
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Gaps

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Indels

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Search completed: February 8, 2002, 15:46:05 Job time: 114 sec

gallus gall saccharomyc homo sapien rattus norv mus musculu escherichia homo sapien homo sapien candida alb drosophila rattus norv rattus norv

Q98936 P38148 P22105 Q62656 Q66556 P76091 P76091 P73078 P23471 P43078 P43078 P43078 P73078 P73078 P73078 P73078 P73078

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PTPG_CHICK
YB9T_YEAST
TENX_HUMAN
PTPZ_RAT
IDUA_MOUSE
                                   YNBD_ECOLI
MJD1_HUMAN
PTPZ_HUMAN
PTPX_CANAL
SEST_DROME
MYSB_RAT
PTN1_RAT
777728
66.99
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83.5
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78.5
; Search time 11.67 Seconds
(without alignments)
691.196 Million cell updates/sec
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                              8, 2002, 15:42:06
                                  protein search, using sw model
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ALIGNMENTS

......VQQRRRSQRQDGEEEDGREL

US-09-847-519A-2 1161 1 MTSGEVKTSLKNAYSSAKRL.

score:

Sequence: Title: Perfect

February

protein

Run on:

, Gapext 0.5

BLOSUM62 Gapop 10.0 ,

Scoring table:

		RESU	RESULT 1
Searched:	100059 seqs, 36664827 residues	DUS3	DUS3_HUMAN
		ID	DUS3_HUMAN STANDARD; PRT; 185 AA.
Total number o	Total number of hits satisfying chosen parameters: 100059	AC	P51452;
		DŢ	01-OCT-1996 (Rel. 34, Created)
Minimum DB seq	Minimum DB seq length: 0	DŢ	01-OCT-1996 (Rel. 34, Last sequence update)
Maximum DB seq	length: 2000000000	ŢĠ	20-AUG-2001 (Rel. 40, Last annotation update)
		DE	DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16)
Post-processin	Post-processing: Minimum Match O%	DE	(DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).
	Maximum Match 100%	CN	DUSP3 OR VHR.
	Listing first 45 summaries	so.	Homo sapiens (Human).
		႘.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Database :	SwissProt_39:*	,S.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		X O	NCBI_TaxID=9606;
Pred. No	Pred. No. is the number of results predicted by chance to have a	RN	[1]
score gr	score greater than or equal to the score of the result being printed,	ŘР	SEQUENCE FROM N.A.
and is d	and is derived by analysis of the total score distribution.	RX	MEDLINE=93101689; PubMed=1281549;
		RA	Ishibashi T., Bottaro D.P., Chan A., Miki T., Aaronson S.A.;
	SUMMARIES	RT	"Expression cloning of a human dual-specificity phosphatase.";
	æ	RL	Proc. Natl. Acad. Sci. U.S.A. 89:12170-12174(1992)

;	COOK STATE
RN	[1]
ŘР	SEQUENCE FROM N.A.
RX	MEDLINE=93101689; PubMed=1281549;
RA	Ishibashi T., Bottaro D.P., Chan A., Miki T., Aaronson S.A.;
RT	"Expression cloning of a human dual-specificity phosphatase.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:12170-12174(1992).
RN	(2)
RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX	MEDLINE=96243129; PubMed=8650541;
RA	Yuvaniyama J., Denu J.M., Dixon J.E., Saper M.A.;
RT	"Crystal structure of the dual specificity protein phosphatase VHR.";
RL	Science 272:1328-1331(1996).
ဗ	-! - FUNCTION: THIS PROTEIN SHOW BOTH ACTIVITY TOWARD TYROSINE-
2	PROTEIN PHOSPHATE AS WELL AS WITH SERINE-PROTEIN PHOSPHATE.
	-! - CAŢALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O -
8	PROTEIN TYROSINE + ORTHOPHOSPHATE.
ყ	-! - SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
8	TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
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ខ	This SWISS-PROT entry is copyright. It is produced through a collabore
ဗ	between the Swiss Institute of Bioinformatics and the EMBL outstati
ניט	the European Bioinformatics Institute There are no restrictions on

homo sapien homo sapien rattus norv

homo sapien

Description

a DB

Length

Ouery Match

Score

Result š homo sapien gallus gall homo sapien rattus norv

DUS3_HUMAN DUS4_HUMAN DUS4_RAT DUS5_MOUSE DUS2_HUMAN DUS1_HUMAN DUS1_HUMAN DUS7_RAT DUS7_HUMAN DUS7_HUMAN DUS7_HUMAN DUS7_HUMAN DUS7_HUMAN DUS7_HUMAN

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rattus norv homo sapien

951452 P 951452 P 951452 P 951452 P 951452 P 951452 P 95145 P

mus musculu homo sapien rattus norv homo sapien

DUS8_MOUSE DUS6_HUMAN DUS6_RAT DUS5_HUMAN

346.5 1996.5 1997.5 1884.5 1884.5 1886.5 166.5 166.5 167.5 1

PTP3_CHLEU VHP1_CAEEL YIL3_YEAST DUSC_HUMAN

chlamydomon caenorhabdi saccharomyc homo sapien vaccinia vi caenorhabdi

MSG5_YEAST PVH1_YEAST VH01_VACCV YO42_CAEEL VH01_RACVI VH01_VACCC

saccharomyc saccharomyc orgyia pseu mus musculu

PTP2_NPVOP PTPG_MOUSE PTPG_HUMAN

homo sapien saccharomyc

vaccinia vi variola vir

P34680 P80994 P20495 P33064 O10273 Q05909 P23470

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ InterPro: IPR000340; DS_phosphatase.
InterPro: IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_DVAL; 1.
HQTO-lase; 3D-structure.
ACT_SITE 124 124
SEQUENCE 185 AA; 20478 MW; C1045DD9B226F or send an email to license@isb-sib.ch) EMBL; L05147; AAA3577.1; -. PDB; 1VHR; 20-JUN-96. MIM; 600183; -.

C1045DD9B226FD94 CRC64;

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                                                                                                                                                                                                                                                              88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                                                                                                                                                                                                                                   63 AEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLV 122
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muda M., Boschert U., Smith A., Antonsonn B., Gillieron C., Chabert C., Camps M., Martinou I., Ashworth A., Arkinstall S.; Molecular cloning and functional characterization of a novel mitogen-activated protein kinase phosphatase, MKP-4."; J. Biol. Chem. 272:5141-5151(1997).
                                                                                                                               37 GAFE----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87
                                                                                                                                                                                           3 GSFELSVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNA 62
                                                                                                                                                                                                                                                                                                                                                                                          146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
COAGUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PROSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16)
(MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN TYROSINE + PHOSPHATE.
-!- SUBGELULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                      11;
   29.8%; Score 346.5; DB 1; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN-TYROSINE PHOSPHATASE.
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
F8598CA95AB379B7 CRC64;
                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                    8.2e-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 AA
                                                                  Mismatches
                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF007082; DSPc; 1.
SMART; SM00195; DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta; MEDLINE-97184169; PubMed-9030581;
                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41867 MW;
                                 43.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y08302; CAA69610.1; -
                                                               78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHATASE 4) (MKP-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 ;
                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300134; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DUSP9 OR MKP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUS9_HUMAN
Q99956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase.
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SEQUENCE
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
DUS9_HUMAN
                                                               Matches
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                                                                                                                                               70 ALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYY-RDMDIQYHGVEADDLPTFDLSVFFYPA 128
                                                                                                           DAESEADRDSMSCGLDSEG----ATPPPVGLRASF-----PVQILPNLYLGSARD 218
                                                                                                                                                                                                                       129 AAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRC-VLPNR 187
                                                                                                                                                                                                                                          273 IEFIDEALS-QNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95221370; PubMed-7535768; Guan K.-L., Butch E.; "Isolation and characterization of a novel dual specific phosphatase, HVH2, which selectively dephosphorylates the mitogen-activated
                                       Gaps
                                                                         12 NAYSSAKR--I,SPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEAT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 4 (EC 3.1.3.48) (EC 3.1.3.16)
                                                                                                                                                                      SANLESLAKLGIRYILNVTPNL-----PNFFEKNGDFHYKQIPISDHWSQNLSRFFFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN TYMODINE TOTAL NUCLEAR.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 = PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase.";
J. Biol. Chem. 270:7197-7203(1995).
-!- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
   DB 1;
 16.9%; Score 196.5; DB 30.5%; Pred. No. 9.7e-12
                                     34; Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR001763; Rhodanese_domain.
Pfam; PF00782; DSPC; 1.
Pfam; PF00581; Rhodanese; 1.
SMART; SM00195; DSPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                             188 GFLKQLRELDKQLVQQRRRSQRQ 210
                                                                                                                                                                                                                                                                                                                     EMBL; U21108; AAA85119.1; -.
                                     62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P51452; 1VHR.
                 Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERK1 AND ERK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUSP4 OR VH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602747;
                                                                                                                                                                                                                                                                                                                                                                                                                            DUS4_HUMAN
013115;
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         DUS4_HUMAN
                                                                                                           173
                                                                                                                                                                                 219
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Mus musculus
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Best Local Si
Matches 50
                                                                                                                                             ACT_SITE
SEQUENCE
                                                                                                                           DOMAIN
                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                  RESULT 5
DUS2_MOUSE
 ***** & g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                               117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last anoctation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 4 (EC 3.1.3.48) (EC 3.1.3.16)
(MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE-2) (MAP KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                        P.J.S.;
Structure,
                                                                                                       6
                                                                                     DB 1; Length 394;
                 CH2 A DOMAIN.
CH2 B DOMAIN.
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                        58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression, and regulation.";
J. Biol. Chem. 270:14587-14596(1995).
-i- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Pheochromocytoma;
MEDLINE-95301550; PubMed=7782322;
Misra-Press A., Rim C.S., Yao H., Roberson M.S., Stork
"A novel mitogen-activated protein kinase phosphatase.
                                              BY SIMILARITY.
0603971759B6952E CRC64;
                                                                                    Score 192.5; DB 1
Pred. No. 2.5e-11;
                                                                                                                                                                                                                                                                        395 AA
PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                       29; Mismatches
                                                                                                                                                                                                                1 : | : | | | : |: |: |: 335
310 VKQRRSIISPNFSFMGQLLQFESQVL 335
                                                                                                                                                                                                     177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                       PRT;
                                              280 B
42953 MW;
                                                                                    16.6%;
34.2%;
         Hydrolase; Nuclear protein.
                                                                                                       50; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                           153
                                                                                                                                                                                                                                                                                                                                        PHOSPHATASE-2) (MKP-2)
                  46
138
197
280
394 AA;
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                  DUSP4 OR MKP2
                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                       DUS4_RAT
                                                                                    Query Match
                           DOMAIN
DOMAIN
                                                                                                       Matches
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SFFFFS
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117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerondakis S., Economou C., Grumont R.J.;
"Structure of the gene encoding the murine dual specificity tyrosine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE + ORTHOPHOSHATE.
-!: SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: IN HEMATOPOIETIC TISSUES SUCH AS SPLEEN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DUS2_MOUSE STANDARD; PRT; 318 AA.

005922; 006640;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93206122; PubMed-7681221;
Shohan P., Davis P., Moskaluk C.A., Kearns M., Krutzsch H.,
Siebenlist U., Kelly M.S.
"PRC-1: a_mitogen-induced nuclear protein tyrosine phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY. A90EFFD378A050FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%; Score 192.5; DB 1
34.2%; Pred. No. 2.5e-11;
tive 29; Mismatches 58
                                                                                                                                                                                                                              PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
Hydrolase; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                        CH2 A DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                     Interpro; IPR000340; DS_phosphatase.
Interpro; IPR001763; Rhodanese_domain.
Interpro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129;
MEDLINE=95203877; PubMed=7896276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   threonine phosphatase PAC1.";
Genomics 24:182-184(1994).
                                                                                                          Pfam; PF00782; DSPC; 1.
Pfam; PF00581; Rhodanese; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 259:1763-1766(1993).
AAC52493.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                             154
395
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                                                                                                                                                                                                                                                                                                                                                                                                                                          281
395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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us-09-847-519a-2.rsp

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SEQUENCE FROM N.A.
                                                                                                                                                                                   ERK1 AND ERK2
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Q9PW71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUS4_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 FQEAISFID-SVKNSGGRVLVHCQAGISRSATICLAXLIQSHRVRLDEAFDFVKQRRGVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 FYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELER-----LFWKGSPQYTHVNEVWPKLYI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FCB-1994 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (EC 3.1.3.48) (EC 3.1.3.16)
DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 GSCNHSSDLQGLQACGITAVLNVS-----ASCPNHFEGL-FHYKSIPVEDNQMVEISAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
          SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY: DUAL SPECIFICITY SUBFÂMILY.
                                                                                                                                                                                                                                                                                           PROSITE; PS00383: TYR_HOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2: 1.
PROSITE; PS50056; TYR_PHOSPHATASE_DOLL; 1.
Hydrolase; Nuclear protein; Alternative splicing.
ACT_SITE 261 261
BY SIMILARITY.
VARSPLIC 175 179 GGPVE -> VSDL (IN SHORT ISOFORM).
VARSPLIC 180 318 MISSING (IN REF. 2).
CONFLICT 11 12 CE -> WQ (IN REF. 2).
CONFLICT 20 20 A -> V (IN REF. 2).
SEQUIENCE 318 AA: 34546 MW; A2006ED0FD27E41D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 184.5; DB 1; Length 318; 28.3%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Mismatches
                                                                                                                                                                                         MGD; MGI:101911; Dusp2.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR0001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                       Pfam; PF00581; Rhodanese; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                                     EMBL; L11330; AAA19666.1; -. EMBL; U09268; AAA85136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 SPNFSFMGQLLQLETQVL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 -PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                               P51452; 1VHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUS2_HUMAN
Q05923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
DUS2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene,
                                                                                                     'PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SELECTION: BELONGENS.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                       YI H., Morton C.C., Weremowicz S., McBride O.W., Kelly K.;
"Genomic organization and chromosomal localization of the DUSP2 encoding a MAP kinase phosphatase, to human 2p11.2-q11.";
Genomics 28:92-96(1995).
-i- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE.PHOSPHATE + H(2)O PROTEIN TYROSINE + ORTHOPHOSPHATE.
MEDLINE-93206122; PubMed-7681221;
Rohan P., Davis P., Moskaluk C.A., Kearns M., Krutzsch H.,
Siebenlist U., Kelly K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDD3543C6DE10CA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: IN HEMATOPOIETIC TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.5%; Score 180.5; DB 1
32.2%; Pred. No. 2.7e-10;
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20-AUG-2001 (Rel. 40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 : | |: | |: | |: || 287 VKQRRGVISPNFSFMGQLLQFETQVL 312
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                                                                                                                                                                                                                                              MEDLINE=96070437; PubMed=7590752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L11329; AAAS0779.1; -.
EMBL; U23853; AAA86112.1; -.
HSSP; P51452; IVHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00782; DSPc; 1.
Pfam; PF00581; Rhodanese; 1.
                                                                                                                                         Science 259:1763-1766(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Nuclear protein.
ACT_SITE 257 257
SEQUENCE 314 AA; 34399 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 32.29
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00195; DSPc; 1
SMART; SM00450; RHOD; 1
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4;

314 QVL 316

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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Cell cycle.
DOMAIN 175 367
                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P51452; 1VHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 AA;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                        TISSUE=Foreskin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P51452; 1
MIM; 600714; -
                                                                    DUS1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
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                                         RESULT 8
DUS1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GITALLUVS-----SDCPNHF-EGHYQYKCIPVEDNHKADISSWFMEAIEYID-SVKEC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 CGRVLVHCQAGISRSATICLAYLAMKKRVKLEKAFEFVKQRRSIISPNFSFMGQLLQFES 313
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 HSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 ISPPSSAESLDLGFSSCGT----PLHDQGGPV-----EILPFLYLGSAYHAARRDMLDAL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 LSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKA 79
                                                                                                                                                                                   Fu S.-L., Waha A., Vogt P.K., "Identification and characterization of genes upregulated in cells
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 4 (EC 3.1.3.48) (EC 3.1.3.16)
(MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE-2) (MAP KINASE
                                                                                                                                                                                                                                      -I-FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
ERKI AND ERKZ (BY SIMILARITY).
-I-CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
PROTEIN TYROSINE + ORTHOPHOSPHATE.
-I-SUBCELDULAR LOCATION: NUCLEAR (BY SIMILARITY).
-I-SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY: DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.5%; Score 180; DB 1; Length 375; 30.1%; Pred. No. 3.9e-10; tive 35; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
179290D0C2BEEEF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1. PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CH2 A DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR000340; DS_phosphatase.
InterPro: IPR0001763; Rhodanese_domain.
InterPro: IPR0001837; TYR_phosphatase.
Pfam: PF00781; DSPc: 1.
Pfam: PF00581; Rhodanese: 1.
SMART: SM00195; DSPc: 1.
                                                                                                                                                            STRAIN-White leghorn;
MEDLINE-20379359; PubMed-10918612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF167296; AAD46656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41052 MW;
                                                                                                                                                                                                               transformed by v-Jun.";
Oncogene 19:3537-3545(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similaricy
nes 55; Conservative
                                                                 Gallus gallus (Chicken).
                                        PHOSPHATASE-2) (MKP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
178
361
375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q16828; 1MKP
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=9031;
                                                    DUSP4 OR MKP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                        Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein tyrosine phosphatase.";
Nature 359:644-647(1992).
-! FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
-: FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
KINASE ERK2 ON BOTH THR-183 AND TYR-185.
-! CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
PROTEIN TYROSINE + ORTHOPHOSPHATE.
-! INDUCTION: BY OXIDATIVE STRESS AND HEAT SHOCK.
-! SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 GHYQYKSIPVEDNHKADISSWFNEAIDFID-SIKNAGGRVFVHCQAGISRSATICLAYLM 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                  (EC 3.1.3.16)
PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                        Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93024952; PubMed-1406996;
Keyes S.M., Emslie E.A.;
"Oxidative stress and heat shock induce a human gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.6%; Score 169; DB 1; Length 367; 30.2%; Pred. No. 4.5e-09; ive 33; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 BY SIMILARITY.
39297 MW; 11BD1D39A9FCD51F CRC64;
                                                                01-DEC-1992 (Rel. 24, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48)
(MAP KINASE PHOSPHATASE-1) (MKP-1) (PROTEIN TYROSINE
CLIOO) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH1).
DUSPI OR PTPNIO OR MKPI OR CLIOO OR VHI.
   367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
PROSITE; PSS0054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPc; 1.
Pfam; PF00581; Rhodanese; 1.
SMART; SM00195; DSPc; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X68277; CAA48338.1; -. PIR; S29090; S29090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 30.2% les 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sp
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EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                          PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                       |: | ||:| | : | : | : | : | ELLPFLYLGSAYHASKCEFLANLHITALLNVSRRTSEACT-----THLHYKWIPVEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                DUS7_RAT
                                                                                                                                                                                                                                             10
                                                                        117
 57
                                                                                                                                                                                                                                                                 DUS7_RAT
                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license eigenement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                Hevroni D., Rattner A., Bundman M., Lederfein D., Gabarah A., Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T., Seger K., Theill L.E., Nedivi E., Richter-Levin G., Citri Y., "Hippocampal plasticity involves extensive gene induction and multiple cellular mechanisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOWARD TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CH2 A DOMAIN.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol. Neurosci. 10:75-98(1998).
-i- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTE: PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE + ORTHOPHOSPHATE.
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
SIMILARITY: CONTAINS THE CDC25 HOMOLOGY DOMAINS 2 A AND B (CH2
DOMAINS A AND B).
                                                                                                                                                                       20-AUG-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 168.5; DB 1; Length 384; 31.5%; Pred. No. 5.3e-09; Live 25; Mismatches 66; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
5644069BBD348700 CRC64;
                   164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50065; TYR_PHOSPHATASE_2; 1. PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1. Hydrolase; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY.
CH2 B DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR00187; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
Pfam; PF00381; Rhodanese; 1.
SMART; SM00195; DSPC; 1.
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98364306; PubMed-9699150;
                                                                                                                                                               38, Created)
38, Last sequ
40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW:
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                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
180
263
384 AA;
                                                                                                                                                             15-JUL-1999 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
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                                                                                                             DUS5_RAT
                                                                                         RESULT
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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234 HTADISSHFQEAIDFID-CVREEGGKVLVHCEAGVSRSPTICMAYLMKTKQFRLKEAFEY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGEEEDYCTPGAFELERLFWKGSP----QYTHVNEVWPKLYIG--DEATALDRYRLQKAG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC 3.1.3.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY; TISSUE-Neuron; MEDLINE=96224012; PubMed=8626780; Muda M., Boschert U., Dickinson R., Martinou J.C., Martinou I., Camps M., Schlegel W., Arkinstall S.; "MKP-3, a novel cytosolic protein-tyrosine phosphatase that exemplifies a new class of mitogen-activated protein kinase phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTYOSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 271:4319-4326(1996).
-1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0
PROTEIN TYROSINE + PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EDUAL SPECIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y SIMILARITY.
45D6F4A92F2BBDDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00782; DSPc; 1.
SMART; SM00195; DSPc; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 166; DB 1; ilarity 31.2%; Pred. No. 6.2e-09; Conservative 29; Mismatches 65
                                                                                                                                                                                                                                                                                                             280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                    293 IKQRRSVVSPNFGFMGQLLQYESEIL 318
                                                                                  177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 E
30668 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X94186; CAA63896.1; -. HSSP; P51452; 1VHR.
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
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9

3;

Gaps

6

Best Local Similarity 31.5 Matches 46; Conservative

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---HGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFI 132
                                                                                                                                        DRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRC-VLPNRGFLK 191
                                                                                                                                                                 221 DEARS-KKCGVLVHCLAGISRSVTVTVAYLAQKANLSLNDAYDFVKRKKSNISPNFNFMG 279
  DGESDRELPSSATESD-----GSPVPSSQPAFPVQILPYLYLGCAKDSTNLD--VLGKYG 173
                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                  || : :: |
280 QLLDFERTL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                              FTHVLNAA - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                   QLRELDKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                 DUS1_MOUSE
P28563;
                                                                                                                                                                                                                                                                                                                                                   RESULT 12
DUSI_MOUSE
                                                                                                                                                                                                                                   192
                                              81
                                                                                                                                        133
                                                                              do do do do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseefisb-sib.ch).
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م
                                                                                                                                   DGESDRELPSSATESD----GSPVPSSQPAFPVQILPYLYLGCAKDSTNLD--VLGKYG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyst1,
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NUV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16)
DUSP7 OR PYST2.
                                           81 FTHVLNAA------HGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFI
                                                                                       132 IKYILNVTPNLPNAFEHG-----GEFTYKQIPISDHWSQ-----NLSQFFPEAISFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
PROTEIN TYROSINE + PHOSPHATE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S., Keyse S.M.;
1 RK/p38 kinases by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 166; DB 1; Length 322; 31.2%; Pred. No. 7.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y SIMILARITY.
E89B1C2ABB2E75DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00105; DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NBG.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., "Differential regulation of the MAP, SAP and RK a novel cytosolic dual-specificity phosphatase. EMBO J. 15:3621-3632(1996).
                                                                                                                                                                                                                                                                                                                                                                                               322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96312959; PubMed-8670865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X93921; CAA63814.1; -. HSSP; P51452; 1VHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00782; DSPc; 1.
SMART; SM00195; DSPc; 1
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322 AA;
                                                                                                                                                                                                                                                             11 : : 1
238 QLLDFERTL 246
                                                                                                                                                                                                                                192 QLRELDKQL 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                          DUS7_HUMAN
Q16829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
SEQUENCE
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EGEEEDYCTPGAFELERLFWKGSP----QYTHVNEVWPKLYIG--DEATALDRYRLQKAG 80

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93360956; PubMed=8355678;
Noguchi T., Metz R., Chen L., Mattei M.-G., Carrasco D., Bravo R.;
"Structure, mapping, and expression of erp, a growth factor-inducible gene encoding a nontransmembrane protein tyrosine phosphatase, and effect of ERP on cell growth.";
Mol. Cell. Biol. 13:5195-5205(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92158357; PubMed-1741163; Charles C.H., Abler A.S., Lau L.F.; "CDNA sequence of a growth factor-inducible immediate early gene and characterization of its encoded protein."; Oncogene 7:187-190(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 75:487-493(1993).
--- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP KINASE EREO ON BOTH THR-183 AND TYR-185.
--- CATALITIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 - PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase in vivo.";
                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48) (EC 3.1.3.16)
MAP KINASE PHOSPHATASE-1) (MAP-1) 
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- INDUCTION: BY GROWTH FACTORS.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94037096; PubMed-8221888; MEDLINE-94037096; PubMed-8221888; Sun H., Charles C.H., Lau L.F., Tonks N.K.; MKP-1 (3CH134), an immediate early gene product, is a dual specificity phosphatase that dephosphorylates MAP kinase in Cell 75:487-493(1993).
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367
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S24411; S24411
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IPR000340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DUS8_HUMAN
              InterPro;
                            InterPro;
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                             275
                                                                                                                                                                                                                                                                                                                                                                                                                                               DUS8_HUMAN
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                                                                                                                                                                                                                                                                                                   44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                             168 LYDQGGPV-----EILSFLYLGSAYHASRKDMLDALGITALINVS-----ANCPNHF-E 215
                                                                                                                                                                                                                                                                                                                                                     104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTHIN PHOSPHATASE 1 (EC 3.1.3.48) (EC 3.1.3.16)
(MAP KINASE PHOSPHATASE-1) (MKP-1) (PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                 14.3%; Score 166; DB 1; Length 367; 30.2%; Pred. No. 8.8e-09; ive 32; Mismatches 65; Indels
                                                                                                                                                                      PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                           50B5F90FEBBD19AB CRC64;
                                                                                                                                                                                                C->S: LOSS OF ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                        164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                 RTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AA
                                                                                     SMART; SM00195; DSPC; I.
SMART; SM00450; RHOD; I.
PROSITE; PS00038; TYR_PHOSPHATASE_1; I.
PROSITE; PS50056; TYR_PHOSPHATASE_2; I.
PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; I.
         MGD; MGI:105120; Ptpn16.
InterPro; IPR000140; DS_phosphatase.
InterPro; IPR0001763; Rhodanese_domain.
InterPro; IPR000187; TR_phosphatase.
Pfam; PF00782; DSPc; 1.
                                                                                                                                                                                                           MW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X84004; CAA58828.1; -. HSSP; P51452; 1VHR.
                                                                                                                                                                                                           39369
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.29
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                      Hydrolase; Cell cycle
DOMAIN 175 367
                                                                                                                                                                                             258
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                                                                 ACT_SITE
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUS1_RAT
Q64623;
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CL100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inactivates mitogen-activated protein kinase.";
J. Neurochem. 65:1823-1833(1995).
-!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN TYROSINE + ORTHOPHOSPHATE.
-!- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274
                                                                                                                                                                                                                                                                                                                                                                                                                                         44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLOKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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SEQUENCE FROM N.A.

MEDLINE-96009533; Pubmed-7561881;

Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E.;

Martell K.J., Seasholtz A.F., Flank S.P., Clemens K.K., Dixon J.E.;

"hVH-5: a protein tyrosine phosphatase abundant in brain that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 013202;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC.3.1.3.48) (EC.3.1.3.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 GHYQYKSIPVEDNHKADISSWFNEAIDFID-SIKDAGGRVFVHCQAGISRSATICLAYLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
-!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 166; DB 1; Length 367; 30.2%; Pred. No. 8.8e-09;
                                                                                                                                                                                                                                         PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                           BY SIMILARITY;
5112ADF290499139 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH-5).
DUSPB OR VH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                 Pfam; PF00781; DSPC: 1.
Pfam; PF00781; DSPC: 1.
SMART; SM00195; DSPC: 1.
SMART; SM00195; DSPC: 1.
SMART; SM00450; RHOD; 1.
PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                              32; Mismatches
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DS_phosphatase.
Rhodanese_domain.
                  IPR001763; Rhodanese_domain
IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                    39541 MW;
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                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 30.2
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                Hydrolase, Cell cycle—DOMAIN 175 367
ACT_SITE 258 258
SEQUENCE 367 AA; 39
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-----LPTFDLSVFFYPAAAFIDRA-LSDDHSKILVHCVMGRSRSATLVLAYLMIHKD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 VNEVWPKLYIGDEATALDRYRLOKAGFTHVLNAAHGRWNVDTGPDXYRDMDIQYHGVEAD 114
                                                                                                                                                                                                                                                                                                                                                                                                        CH2 A DOMAIN.
CH2 B DOMAIN.
PROTEIN-TYROSINE PHOSPHATASE.
POLY-ARG.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
416F429A12C1FA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 163; DB 1;
Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 MTLVDAIQQVAKNR-CVLPNRGFLKQLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: || : | | : | | 267 MSSDDAYRFVKDRRPSISPNFNFLGQLLEYERSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Mismatches
                                                                                                                                                                                                                                                                                                                     PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_2; 1. PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8, 2002, 15:45:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY.
POLY-SER.
PRO-RICH.
                                                                                                                                                                       MGD; MGI:106626; Nttpl.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR001763; Rhodanese_domain.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
SMART; SM00195; DSPC; 1.
SMART; SM00450; RHOD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ĭ.,
                                                                                                                                              EMBL; X95518; CAA64772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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ne: 190 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96311565; PubMed=8733137;
Theodosiou A.M., Rodrigues N.R., Nesbit M.A., Ambrose H.J.,
Theodosiou A.M., Rodrigues N.R., Nesbit M.A., Ambrose H.J.,
Baterson H., McLellan -Arnold E., Boyd Y., Leversha M.A., Owen N.,
Blake D.J., Ashworth A., Davies K.E.;
"A member of the MAP kinase phosphatase gene family in mouse
containing a complex trinucleotide repeat in the coding region.";
Hum. Mol. Genet. 5:675-684(1996) SOTH ACTIVITY TOWARD TYROSINE-PROTEIN
PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEAD 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Last sequence update)
C-AUG-2001 (Rel. 40, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 3.1.3.16)
(NEURONAL TYROSINE THREONINE PHOSPHATASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: CYTOPIASMIC AND NUCLEAR.
-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN AND LUNG.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 163; DB 1; Length 625; 32.5%; Pred. No. 3.4e-08; tive 30; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O PROTEIN TYROSINE + PHOSPHATE.
                                                                                                                                                                                                                                                                           CH2 A DOMAIN.
CH2 B DOMAIN.
PROTEIN-TYROSINE PHOSPHATASE.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
DCBEA14487219666 CRC64;
               InterPro: IPR000340; DS_phosphatase.
InterPro: IPR001965; P_ICh_extensn.
InterPro: IPR001963; Rhodanese_domain.
InterPro: IPR001763; Rhodanese_domain.
InterPro: IPR001763; TYR_phosphatase.
Pfam; Pr00782; DSPC: 17R_phosphatase.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00450; RHOD; 1.
PROSITE; PS000383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; IPROSITE; PS50056; TYR_PHOSPHATASE_2; IPROSITE; PS00056; TYR_PHOSPHATASE_DAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663 AA.
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(Rel. 38, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                      65840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUSP8 OR NTTP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                      DOMAIN
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7:

22;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-847-519A-2 1161 1 WTSGEVKTSLKNAYSSAKRL......VQQRRRSQRQDGEEEDGREL 220 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

Database :

pirl:* pir2:* pir3:* pir4:* PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	dual specificity p	hypothetical prote		dual specificity p	specifi	dual specificity p	dual specificity p	ein tyro	cifí	protein tyrosine p	thetical	dual specificity p	dual specificity p	dual specificity p	probable protein p	protein tyrosine p	dual specificity p	hypothetical prote		ຜ	hypothetical prote	hypothetical prote	ble dual	dual specificity p	phosphatase-like p	protein-tyrosine-p	dual specificity p	hypothetical prote	probable dual spec
SUMMARIES	ΩI	A47196	T32494	T46405	A56947	A56115	B57126	A57126	149365	S29090	149364	T21380	S24411	S52265	T03074	G84458	T39698	138890	T16056	T18915	T48906	T17802	T15969	S48459	S58725	T47666	S31304	QQVZH1	S41012	T30684
	DB	П	~	7	~	7	7	-	~	П	7	7	П	~	~	7	7	-	7	~	7	7	~	-	-	~	Н	П	7	7
	Length	185	365	303	393	394	314	314	223	367	202	226	367	367	142	283	330	384	186	272	276	204	619	209	489	771	364	171	292	169
æ	Ouery Match	29.8	17.6	16.6	16.6			•	15.0	•	14.5	•	14.3	•		13.7	13.6	13.6	13.0	11.8	11.8	11.6	11.4	11.4	10.7	•	10.5	•		•
	Score	346.5			192.5			180.5	174	169	168	168	166	166	160.5	159	158	157.5	150.5	137	136.5	134.5	132.5	132	124.5	124	122	113		110.5
	Result No.	7	73	٣	4	2	ø	7	6 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

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Indels 11; Gaps

Length 185;

37 GAFE-----LERLFWKGSPQYT----HVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNA 87

Query Match 29.8%; Score 346.5; DB 1; Best Local Similarity 43.8%; Pred. No. 1.2e-24; Matches 78; Conservative 35; Mismatches 54;

dual specificity p	dual specificity p	dual specificity p	probable dual spec	JlL protein - vari	dual-specificity M	protein tyrosine p	protein-tyrosine-p	prenylated protein	hypothetical prote	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	conserved hypothet	protein-tyrosine-p	hypothetical prote
B47452	A42514	I36845	T28522	B72161	T39517	T10278	B48148	JC5982	T19418	A48148	S56283	T42636	D83329	A56059	F84771
-	٦	7	7	~	~	7	-	7	~	-	~	~	~	7	7
171	171	171	171	171	278	1.60	1442	173	272	1445	551	1422	437	173	383
9.3	9.5	9.1	9.1	9.1	8.7	8.4	8.4	8.3	8.1	8.1	7.8	7.8	7.8	7.3	7.3
108	107	106	106	106	101.5	86	97.5	96.5	93.5	93.5	91	91	90	82	82
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1	
	À47196	
	dual specificity phosphoprotein phosphatase (EC 3.1.3) DUSP3 [validated] - human	
	N.Alternate names: protein tyrosine-phosphatase VHR; VH1-related dual-specificity ph	~
	Cispecies: Homo sapiens (man)	
	C:Date: A.1-Sep-1994 #Sequence_revision Ol-Mar-1990 #text_cnange 13-Sep-2000 C:Accession: A41106: A58760	
	Residentiabacht T. Rottaro D. Chan. A. Mikt. T. Aarongon. S. A.	
	Proc. Nate Acad Sci. U.S.A. 89, 12170-12174, 1992	
	A: Title: Expression cloning of a human dual-specificity phosphatase.	
	A) Reference number: A47196; MUID:93101689	
	A/ACCESSION: A4/1190 A/ACCESSION: A5/1190	
	A:Residues: 1-185 <lsh></lsh>	
	A;Cross-references: GB:L05147; NID:g181839; PIDN:AAA35777.1; PID:g181840	
	A, Experimental source: fibroblasts	
	A; Note: sequence extracted from NCBI backbone (NCBIN:120790, NCBIP:120791)	
	(R:Denu, J.M.; Zhou, G; Wu, L.; Zhao, R.; Yuvaniyama, J.; Saper, M.A.; Dixon, J.E.	
	使き BIOL: CAGH. S.7(y, 3/20-3604) 1990 でき BIOL: CAGH. S.7(y, 3/20-3604) 1990 第一年10-1990 onveiled on and characterization of a human dual-special fit orditola furn	
	A:Reference number: A58760: MUID:95181338	١.
	A; Accession: A58760	
	A; Molecule type: protein	
	A; Residues: 2-7 <den></den>	
	R:Yuvaniyama, J.; Denu, J.M.; Dixon, J.E.; Saper, M.A.	
	Submitted to the Brookhaven Protein Data Bank, February 1996	
	A/Relefance unimper: A000.27, FUBI.LVMR A/Contents: annotation: X-ray crystallography 2 1 angstroms residues 8-185	
	or o compress transfer test the	
	j. Biol. Chem. 269, 28084-28090, 1994	
	A; Title: The catalytic role of Cys(124) in the dual specificity phosphatase VHR.	
	A; Reference number: A55447; MUID:95050584	
	A.Contents: annotation; active site	
	ictemetics: vub	
	A.Gene. Obs.Costs., vin. A.Gree-references (DR-342110, OMIM.600183	
	A: Map bosition: 17921-17921	
	C; Function:	
	A; Description: catalyzes hydrolysis of peptidyl-phosphoserine, -phosphothreonine and	773
	C; Superiamily: dual specificity phosphoprotein phosphatase DUSP3; VH1-type dual spec	F 1
	C. Keywords: phosphopicuent, phosphoric monoester hydrolase	
	F;37-177/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <vh1:< td=""><td></td></vh1:<>	
	F:124/Active site: Cys (phosphocysteine intermediate) #status experimental F:130/Binding site: substrate phosphate (Arg.) #status predicted	
1	trico bringing since broading () "standing broading	

us-09-847-519a-2.rpr

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58;
      29; Mismatches
                                                                                                                                                                                                          201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
        Conservative
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A; Residues: 1-394 <GUA>
      50;
                                            57
                                                                                                                           117
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      Matches
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C;Genetics:
A;Note: DKF2p43401321.1
C;Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF036685; PIDN:AAB88308.1; GSPDB:GN00022; CESP:C05B10.1 A;Experimental source: strain Bristol N2; clone C05B10 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                 hypothetical protein C05B10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct.1999 #sequence_revision 29-Oct.1999 #text_change 29-Oct.1999
C;Accession: T3494
R;Geisel, C.; Wamsley, P.
submitted to the RmL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C05B10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
T46405
T46405
T46405
T6405
T6405
T6405
T6705
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C;Accession: T46405
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223034
                                                           88 AHGR--WNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILV 145
                                                                                     63 AEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRYLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 SVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAK-N 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 TKFFPEAISFIDDARRND-SACLVHCLAGISRSVTICLAYLMKTEMCTLDSAYEWVQKRN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDL 121
146 HCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 4
A;Introns: 22/2; 46/2; 74/3; 163/2; 204/2; 248/1; 287/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.6%; Score 204.5; DB 2; 38.6%; Pred. No. 3.4e-11; tive 24; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: T32494
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <GEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RCVLPNRGFLKQLRELDKQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 ASIAPNFHFMGOLTDYEKML 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-303 <AAA>
A;Cross-references: EMBL:AL137704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.6%
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T46405
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: C05B10.1
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Length 303;

Score 192.5; DB 2; Pred. No. 3.4e-10;

16.6%; 34.2%;

Query Match Best Local Similarity

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C;Accession: A56947
R:Misra-Press, A.; Rim, C.S.; Yao, H.; Roberson, M.S.; Stork, P.J.S.
J. Biol. Chem. 270, 14587-14596, 1995
A;Title: A novel mitogen-activated protein kinase phosphatase. Structure, expression: A;Reference number: A56947; MUID: 95301550
A;Accession: A56947
A;Accession: A66947
A;Accession: A66947
A;Accession: A66947
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A;Accessio
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4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dual specificity phosphatase (EC 3.1.3.-) HVH2 - rat
N.Alternate names: mitogen-activated protein kinase phosphatase 2
C.Species: Rattus norvegicus (Norway rat)
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-1999
C.Accession: A56947
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                                                                                                           EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                       PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                          57 EVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQ 176
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Indels
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C,Genetics:
GGene: GB:UDSP4; HVH2; MKP-2
A,Cross-references: GDB:433893
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us-09-847-519a-2.rpr

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H.; Slebenlist,

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A Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine C; Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specific C; Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase F; 140-160/Region: nucleus; pacation signal F; 180-311/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1 F; 257/Active site: Cys (phosphocysteine intermediate) #status predicted F; 263/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein tyrosine phosphatase - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Spate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 (Spates) (Spa
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C;Superfamily: VH1-type dual specificity phosphoprotein phosphatase homology
F;36-174/Domain: VH1-type dual specificity phosphoprotein phosphatase homology
                                                                                            Chacassion: A57126
Richan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Krutzsch, H.; Slebenlis Science 259, 1763-1766, 1993
A; Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase. A; Reference number: A57126; MUID: 93206122
A; Reference number: A57126; MUID: 93206122
A; Status: nucleic acid sequence not shown A; Cross-references: GB: L11329; NID: 9559539; PIDN: AA50779.1; PID: 9292376
C; Genetics: A; Genetics: A; Armap position: 2411-2411
                   C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1999
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Best Local Similarity 32.2%
Matches 47; Conservative
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Matches 55; Conserv
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A57126
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - human
N:Alternate names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activate
                                                                   phosphatase 1; VH1-type dual specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kel
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C:Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificit
C:Keywords: nucleus: phosphoprotein: phosphoprotein phosphatase en with trippe dual specificity phosphoprotein phosphatase homology <VH1>
F:180-311/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F:257/Active site: Cys (phosphocysteine intermediate) #status predicted
F:263/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                           homology <VH1>
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N.Alternate names: mitogen-induced nuclear protein-tyrosine-phosphatase PAC-1
C.Specias: Mus musculus (house mouse)
C.Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Apr-1998
C.Accession: B57126
R.Rohan, P.J.: Davis, P.; Moskaluk, C.A.; Kearns, M.; Krutzsch, H.; Siebenlist Aritie: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
A.Reference number: A57126; MUID:99206122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNRCVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELER----LFWKGSPQYTHVNEVWPKLYI 64
A:Map position: 8p21-8p11.2
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type d
C:Superfamily: dual specificity phosphoric monoester hydrolase
F:203-334/Domain: VH1-type dual specificity phosphorotein phosphatase h
F:280/Active site: Cys (phosphocysteine intermediate) #status predicted
F:286/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EILPFLYLGSAYHAARRDMLDALGITALLNVS-----SDCPNHF-EGHYQYKCIPVEDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 394;
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                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                     16.6%; Score 192.5; DB 2 34.2%; Pred. No. 4.8e-10; ive 29; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 VAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
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Best Local Similarity 34.2'
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Conservative
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: mRNA
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<VH1;

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A)Cross-references: EMBL:U34973; NID:g1063624; PIDN:AAA87036.1; PID:g1063625
C;Superfamily: VHI-type dual specificity phosphoprotein phosphatase homology
F;36-174/Domain: VHI-type dual specificity phosphoprotein phosphatase homology <VHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - mouse N:Alternate names: 3CH134 protein; protein-tyrosine-phosphatase erp, nonreceptor typ
                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F26A3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21380
R;McMurray, A.
submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 GFTHVLNAAHGRWNVDTG---PDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 M-DIQYHGVEADDLPTFDLSVFFYPAAAFID---RALSDDHSKILVHCVMGRSRSATLVL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYLMIHKDMTLVDAIQQV-AKNRCVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEEDGR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYR--LQKA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 SDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNR-CVLPNRGFLKQLR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                              ----PMRREMQEVLPGLFLGPYSSAMKSKLPILQKH
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                                                                                                                                                                                                                                                                                                           , 19
                                                                                                                                                                                                                                                       14.5%; Score 168; DB 2; 30.2%; Pred. No. 3.8e-08; iive 30; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 168; DB 2; 30.8%; Pred. No. 4.3e-08; ive 35; Mismatches 73
                  A; Accession: 149364
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-205 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: 219415
A; Accession: T21380
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DPA
A; Residues: 1-256 cMIL>
A; Cross-references: EMBL:278419; PIDN:CAB01700.1; G;
  number: 149364; MUID:96070766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Map position: 1
A:Introns: 117/2; 150/3; 186/3
                                                                                                                                                                                                                                                                              Local Similarity 30.2 hes 54; Conservative
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Best Local Similarity 30.8
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        12 POCKDDAEEWTY-----
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QL 171
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                                                                                                                                                                                                                                                                                                RESULT 9
30900
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - human
N.Alternate names: protein tyrosine-phosphatase CL100; protein tyrosine-phosphatase, nor
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 15-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
C.Accession: 829090; A53052
S.M.: Emslie, E.A.
Nature 359, 644-647, 1992
A.Title: Oxidative stress and heat shock induce a human gene encoding a protein-tyrosine
A.Reference number: 829090; MUID:93024952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S29090
A; Molecule type: mRNA
A; Molecule type: marka
A; Molecule type: martell, K.J.; Dixon, J.E.
B; Kwak, S.P.; Hakes, D.J.; Martell, K.J.; Dixon, J.E.
A; Title: Isolation and characterization of a human dual specificity protein-tyrosine phota R; Reference number: A53052; MUID:94148864
A; Accession: A53052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein tyrosine phosphatase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession : 149364
R;Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
J. Biol. Chem. 270, 26782-26785, 1995
A;Title: A single mutation converts a novel-phosphotyrosine binding domain into a dual-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: GDB:136197; OMIM:600714
A; Map position: 5934-5934
C; Superfamily: dual specificity phosphorotein phosphatase 1; VH1-type dual specificity
C; Keywords: heat shock; phosphorotein; phosphoric monoester hydrolase; stress-induced F; 181-312/Domain: VH1-type dual specificity phosphorotein phosphatese homology <VH1>F; 258/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 264/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: sequence extracted from NCBI backbone (NCBIN:143800, NCBIN:143802, NCBIN:143804 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                                                   56 GITHIICI---RONIEANPIKPNF--OOLFRYLVLDIADNPVENIIRFFPMTKEFIDGSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 GHYQYKSIPVEDNHKADISSWFNEAIDFID-SIKNAGGRVFVHCQAGISRSATICLAYLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 RTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 169; DB 1;
; Pred. No. 6.4e-08;
33; Mismatches 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.6%;
30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: leukòcyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 30.29
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: DUSP1; PTPN10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-367 < KWA>
                                                                                                                                                                         196 LD 197
                                                                                                                                                                                                                          170 YE 171
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C. Accession: T03074
R. Bahr, U.; Tidona, C.A.; Darai, G.
Wirus Genes 15, 235-245, 1997
Wirus Genes 12, 235-245, 1997
Wirus Genes 1000
Wirus Genes I 14834; MuID:98141693
Wirus Genes I 14834; MuiD:98141693
Wirus Genes I 1482
Wirus Genes I 1482
Wirus Genes I 1482
Wirus Genes Ge
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C;Species: Arabidopsis thaliana (mouse-aer cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84458
R;Lin, X:, Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallor euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:2008348?
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Chilo iridescent virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dual specificity phosphoprotein phosphatase homolog - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar=1999 #sequence_revision 24-Mar=1999 #text_change 08-Oct=1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 YSHLQKVTTLIHDSI-ENGNKVLVHCQAGISRSATVVIAYIMRSKRYSLQDAFNFVKKKR 115
                      44 LFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRD 103
                                                                                                                                                                                            104 MDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLM 163
                                                                                                                                                                                                                                                   LYIGDEATALDRYRLQKAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVFFYPAAAFIDRALSDDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LYLGNIQNGI---RHSNYGFDKIINLT--RFNNQYG------IPTVWINIDDSESSDL 56
                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable protein phosphatase [imported] - Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.8%; Score 160.5; DB 2; 32.9%; Pred. No. 1.2e-07; tive 24; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                           164 IHKDMTLVDAIQQVAKNRCVL-PNRGFLKQLRELDKQLV 201
                                                                                                                                                                                                                                                                                                                                                                                                                             :: || ||:||| ::: |
116 SIIFPNAGFIKQLAQFERWL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVL-PNRGFLKQLRELDKQL 200
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-283 <S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: At2g04550
A: Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A: Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                   216
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    . S., a
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A;Cross_references: GB:S64851; NID:g409976; PIDN:AAB27882.1; PID:g409977
B;Charles, C. H.; Abler.
A. R.; Abler.
A. 187-190, 1992
A. Title: cDNA sequence of a growth factor-inducible immediate early gene and characteriz
A;Reference number: S24411
A;Molecule type: mRNA
A;Residues: 1.367 ACHA>
A;Cross_references: EMBL:X61940; NID:g49735; PIDN:CAA43944.1; PID:g49736
C;Genetics:
A;Gene: erp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity C:Superfamily: dual specificity protein; phosphorotein; phosphoric monoester hydrolase F:B1-312/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>F:258/Active site: Cys (phosphacysteine intermediate) #status predicted F:264/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Cross-references: EMBL:X84004; NID:g642264; PIDN:CAA58828.1; PID:g642265
C.Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
C.Superfamily: dual specificity phosphorotein phosphatase
K.Steywords: phosphoprotein; phosphoric monoester hydrolase
F:181-312/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F:258/Active site: Cys (phosphocysteine intermediate) #status predicted
F:264/Binding site: substrate phosphate (Arg) #status predicted
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N.Alternate_names: protein-tyrosine-phosphatase CL100; protein-tyrosine-phosphatase,
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
C;Accession: A54681; S2441
S2461; S2441
NG1: 12, Metz, R.; Chen, L.; Mattei, M.G.; Carrasco, D.; Bravo, R.
Mol. Cell. Biol. 13, 5195-5205, 1993
A;Title: Structure, mapping, and expression of erp, a growth factor-inducible gene of A;Reference number: A54681; MUID:93360956
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Cispecies: Rattus passaguence_revision 21-Jul-1995 #text_change 22-Jun-1999
Cispecies: Sizelegel, W.; Arkinstall, S.
Submitted to the EMBL Data Library, January 1995
A;Reference number: S32265
A;Reference number: S32265
A;Reference number: S32265
A;Reference number: Norway Regulating CL100 gene expression in pituitary cells.
A;Accession: S52265
A;Reference number: Norway Residues: 1-367 <MUD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 GHYQYKSIPVEDNHKADISSWFNEAIDFID-SIKDAGGRVFVHCQAGISRSATICLAYLM 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.3%; Score 166; DB 2; Length 367; 30.2%; Pred. No. 1.2e-07; 1.ve 32; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 RTNRVKLDBAFEFVKQRRSIISPNFSFMGQLLQFESQVL 313
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Best Local Similarity 30.29
Matches 48; Conservative
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-367 <NOG>
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Gaps

28;

Indels

Length 283;

13.7%; Score 159; DB 2; L 31.1%; Pred. No. 3.8e-07; ive 28; Mismatches 57;

Query Match 13.7 Best Local Similarity 31.1 Matches 51; Conservative

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Gaps

14;

48; Conservative

26 EEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPK-LYIGDEATALDRYRLQ 77 11	78 KAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALS 137	74 TQGISRVLNTVPMCQNLYRN-SFTYHGLDNEKVLQFDDAIKFLDQC-E 119	138 DDHSKILVHCVMGRSRSATLVLAYLMIHKDMTLVDAIQQVAKNR 181	120 KDKARVLVHCMSGKSRSPAVVVAYLMKRKGWRLAESHQWVKQRR 163 ·	
26	78	74	138	120	
Qy Dp	οy	qα	οy	QQ	

Search completed: February 8, 2002, 15:44:07 Job time: 191 sec